OM nucleic - nucleic search, using sw model

Run on: January 30, 2004, 22:33:45 ; Search time 4088 Seconds
             (without alignments)
             11108.044 Million cell updates/sec

Title: US-09-898-456-6
Perfect Score: 1110
Sequence: 1 atgctgtgctgcattcagtg.............tgggtaaggcagtcgcctga 1110

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                1: gb_ba:*
                2: gb_bct:*
                3: gb_in:*
                4: gb_om:*
                5: gb_ov:*
                6: gb_pat:*
                7: gb_ph:*
                8: gb_pl:*
                9: gb_pr:*
                10: gb_ro:*
                11: gb_sts:*
                12: gb_sy:*
                13: gb_un:*
                14: gb_vi:*
                15: gb_vrl:*
                16: gb_fun:*
                17: gb_hum:*
                18: gb_in:*
                19: gb_mu:*
                20: gb_om:*
                21: gb_or:*
                22: gb_ov:*
                23: gb_pat:*
                24: em_ph:*
                25: em_pl:*
                26: em_ro:*
                27: em_sts:*
                28: em_un:*
                29: em_vi:*
                30: em_vrl:*
                31: em_htg_hum:*
                32: em_htg_inv:*
                33: em_htg_other:*
                34: em_htg_mus:*
                35: em_htg_pln:*
                36: em_htg_rod:*
                37: em_htg_mam:*
                38: em_htg_vrt:*
                39: em_sy:*
                40: em_htgo_hum:*
                40: em_htgo_mus:*
                41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	989.6	89.2	1498	9	AB057725	Homo sapi
2	989.6	89.2	1650	9	AX298282	Homo sapi
3	988	89.0	1064	9	AX350382	Sequence
4	974	87.7	1597	9	AY009402	Homo sapi
5	969.4	87.3	1245	6	AX153809	Sequence
6	741.6	66.8	1747	10	MMWNT8DPT	M.musculus
7	708.4	63.8	1245	6	Z68889	M.musculus
8	569.4	51.3	1734	5	AX153811	Sequence
9	547	49.3	149172	9	U02097	Gallus gall
10	547	49.3	166870	9	AC004826	Homo sapi
c	11	542.2	48.8	217608	9	AC113382	Homo sapi
12	537.8	48.5	1749	5	AC148871	Pan trogl
c	13	535	48.2	144402	2	AC021854	Homo sapi
14	533.6	48.1	1598	5	AF308871	Ambystoma
15	477.2	43.0	3022	5	XLKXWNT8	X.laevis Xw
16	454	40.9	1185	5	U10869	Danio rerio
17	436.2	39.3	1994	5	U10870	Danio rerio
18	434.6	39.2	2119	6	AB073637	Homo sapi
19	434.6	39.2	2119	6	AX565733	Sequence
20	434.6	39.2	2119	6	AX597133	Sequence
21	434.6	39.2	2119	9	AX701379	Sequence
22	433	39.0	1634	10	HSWNT8	H.sapiens m
23	417	37.6	71141	9	AF130349	Mus muscu
c	24	415.4	37.4	885	9	AC025365	Homo sapi
25	389	35.0	191880	2	X91940	H.sapiens m
26	389	35.0	254734	2	AC133619	Rattus no
27	384.4	34.6	201643	10	AC134361	Rattus no
28	317.8	28.6	1472	3	AC074335	Mus Muscu
29	306.4	27.6	1516	3	AF206500	Branchios
30	302.6	27.3	1467	5	AF190470	Branchios
31	232.8	21.0	7552	5	XLU22173	Xenopus lae
c	32	232.8	21.0	174835	5	AY032749	Danio rer
33	232.8	21.0	174835	5	BX248097	Danio rer
34	221.4	19.9	435	5	XELXWNT8A	Xenopus lae
c	35	190	17.1	212568	10	M55058	Xenopus lae
c	36	190	17.1	254819	2	AC103018	Rattus no
37	188.2	17.0	138622	10	AC105487	Rattus no
38	186.6	16.8	157808	9	AC124401	Mus muscu
39	186.6	16.8	1068	9	AL133352	Human DNA
40	183	16.5	5177	6	Y11108	H.sapiens W
41	170	15.3	1195	6	HSWNT8BGN	Sequence
42	170	15.3	1195	6	AX695367	Sequence
43	170	15.3	1195	6	AX002047	Sequence
44	170	15.3	1195	6	AX565669	Sequence
45	170	15.3	1195	6	AX597069	Sequence
	170	15.3	1195	6	AX695366	Sequence
	170	15.3	1195	6	AX701349	Sequence
	170	15.3	1195	6	E31300	Novel compo

ALIGNMENTS

RESULT 1
AB057725
LOCUS   AB057725   1498 bp   mRNA   linear   PRI 23-JUN-2001
DEFINITION   Homo sapiens mRNA for WNT8A, complete cds.
ACCESSION   AB057725
VERSION   AB057725.1 GI:14495175
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
  AUTHORS   Saitoh,T. and Katoh,M.
  TITLE   Molecular cloning and characterization of human WNT8A
  JOURNAL   Int. J. Oncol. 19 (1), 123-127 (2001)

```
MEDLINE
PUBMED      21301559
REFERENCE   11408932
AUTHORS     2 (bases 1 to 1498)
            Katoh,M.
TITLE       Direct Submission
JOURNAL     Submitted (19-MAR-2001) Masaru Katoh, National Cancer Center
            Research Institute, Genetics and Cell Biology Section, Genetics
            Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan
            (E-mail:mkatoh@ncc.go.jp, Tel:81-3-3542-2511)
FEATURES             Location/Qualifiers
     source          1..1498
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2"
     gene            1..1498
                     /gene="WNT8A"
     CDS             6..1061
                     /gene="WNT8A"
                     /codon_start=1
                     /product="WNT8A"
                     /protein_id="BAB60960.1"
                     /db_xref="GI:14495176"
                     /translation="MGNLFMLWAALGICAAFSASAWSVNNFLITGPKAYLIYTTSVA
                     LGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATRETSFIHAISSAGVMYIITK
                     NCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALM
                     NLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKI
                     EMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECL
                     QNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKY
                     YCARSPGSAQSLGKGSA"
BASE COUNT      384 a    343 c    426 g    345 t
ORIGIN

Query Match    89.2%;  Score 989.6;  DB 9;  Length 1498;
Best Local Similarity   99.6%;  Pred. No. 1.3e-283;
Matches 992;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy  115 TTTGGTAGGTTCAGTGAACAAATTTCCTGATAATGAGGTCCCAAGGCCTATCTACACACG 174
            ||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   66 TCTCCCTGGTCAGTGAACAAATTTCCTGATAACGAGGTCCCAAGGCCTATCTACACACG 125

Qy  175 ACTAGTGTGGCCTTGGGTGCCCAGAGTGGGCATGAGGAGGTCCAAGTTCCAGTTTGCTTGG 234
            |||||||||||| |||||||||||||||||| ||||||||| |||||||||||||||||||
Db  126 ACTAGTGTGGCCCTTGGGTGCCCAGAGTGGGCATCGAGGAGGTGCAAGTTCCAGTTTGCTTGG 185

Qy  235 GAACGCTGGAACTGCCCTGAAAAATGCTCTTCAGCTCTTCCAACCCACACAGGCTGAGAGT 294
            |||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db  186 GAACGCTGGAACTGCCCTGAAAAATGCTCTTCAGCTCTTCCACCCACAACAGGCTGAGAGT 245

Qy  295 GCTACCAGAGAGAGACTTCCTTCATCACATCGTCTATCAGCTCTGCTGAGTCATGTTACATCATC 354
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  246 GCTACCAGAGAGAGACTTCCTTCATACATGTCTATCAGCTCTGCTGAGTCATGTTACATCATC 305

Qy  355 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAAACAAATGGA 414
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  306 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTCAAACAAATGGA 365

Qy  415 AAAACAGGAGGGCCATGGGTGGATTCTGGGGAGGCTGCAGCGATAATGTGGAATTTGGGGAA 474
            ||||||||||||||||||| |||||||||||||||||||||||| |||||||||||||||||
Db  366 AAAACAGGAGGGCCATGGGCTGGATTCTGGGGAGGCTGCAGCGACAATGTGGAATTTGGGGAA 425

Qy  475 AGGATCTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGCAAGGATGCCAGAGCCCTGATG 534
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  426 AGGATCTCCAAAACTCTTTGTGGACAGTTTGGAGAAGGGCAAGGATGCCAGAGCCCTGATG 485

Qy  535 AATCTTCACAACAACAGGGCGGGCGGAGAGCCACCATGAAAAAGGACATGC 594
            ||||||||||||||||||||||||||| ||||||||||||| |||||||||
Db  486 AATCTTCACAACAACAGGGCGGGCGGCAGAGCCACCATGAAAAGGACATGC 545

Qy  595 AAAGTGTCATGGCATCTCTGGGAGCTGCAGCGACTGCTGCTGGCTGAA 654
            ||| |||||||||||| |||||||||||||||||| ||||||||||||
Db  546 AAAATGTCATGGCATTCTCTGGGAGCTGCAGCGACATGCTGGCTGGCTGAA 605
```

```
Qy  655 TTCCGGGAGATGGGGGAGACTACCTAAAGGCCAAGTATGACAAGGCC 714
            |||||||||||||||||||||||||||||||||||||||||||||||
Db  606 TTCCGGGAGATGGGGGAGACTACCTAAAGGCCAAGTATGACAAGGCC 665

Qy  715 GATAACGCGGCCAGCTGAGAGCTGGGAACAGCGCCCCGCGAGGGCC 774
            |||||||||||||||||||||||||||||||||||||||||||||||
Db  666 GATAACGCGGCCAGCTGAGAGCTGGGAACAGCGCCCCGCGAGGGCC 725

Qy  775 TTCCTTCCTAGCGCAGAGGCGGAACTGATCTTTTTAGAGGAAATCACCAGATTACGTACC 834
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  726 TTCCTTCCTAGCGCAGAGGCGGAACTGATCTTTTTAGAGGAAATCACCAGATTACGTACC 785

Qy  835 TGCAATTCCAGCCTGGGCATCTATGGCCACACAGAGGGTGCCTACACAGCCAC 894
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  786 TGCAATTCCAGCCTGGGCATCTATGGCCACACAGAGGGTGCCTACACAGCCAC 845

Qy  895 AACACATCCAGGTGGGAGCGACGTAGCTGTTGGGCGCCCTGTTGCACTCGAGTGTACGC 954
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  846 AACACATCCAGGTGGGAGCGACGTAGCTGTTGGGCGCCCTGTTGCACTCGAGTGTACGC 905

Qy  955 GTGGAAGAGGAGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCAGTGGTGTGT 1014
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906 GTGGAAGAGGAGAAAACTGAGGTCATAAGCAGCTGTAACTGCAAATTCCAGTGGTGTGT 965

Qy 1015 ACGGTCAAGTGTGACCAGTGTTGTGGTGACACGGCTCCCCA 1074
            |||||||||||||||||||||||||||||||||||||||||
Db  966 ACGGTCAAGTGTGACCAGTGTTGTGGTGACACGGCTCCCCA 1025

Qy 1075 GGCCAGTGCCCAGTCCCTGGGTAAGGGCCAGTGCCTGA 1110
            ||||||||||||||||||||||||||||||||||||||
Db 1026 GGCCAGTGCCCAGTCCCTGGGTAAGGGCCAGTGCCTGA 1061
```

```
RESULT 2
LOCUS       AX298282              1650 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 1 from Patent WO0183543.
ACCESSION   AX298282
VERSION     AX298282.1  GI:17128299
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Duecker,K.
  TITLE     Human wingless-like gene
  JOURNAL   Patent: WO 0183543-A 1 08-NOV-2001;
            MERCK PATENT GmbH (DE)
FEATURES             Location/Qualifiers
     source          1..1650
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             100..1155
                     /codon_start=1
                     /note="unnamed protein product"
                     /protein_id="CAD12696.1"
                     /db_xref="GI:17128300"
                     /translation="MGNLFMLWAALGICAAFSASAWSVNNFLITGPKAYLIYTTSVA
                     LGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATRETSFIHAISSAGVMYIITK
                     NCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALM
                     NLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKI
                     EMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECL
                     QNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKY
                     YCARSPGSAQSLGKGSA"
BASE COUNT      384 a    384 c    460 g    383 t
ORIGIN

Query Match    89.2%;  Score 989.6;  DB 6;  Length 1650;
Best Local Similarity   99.6%;  Pred. No. 1.3e-283;
Matches 992;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
LOCUS       AX350382                1064 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 7 from Patent WO0181578.
ACCESSION   AX350382
VERSION     AX350382.1  GI:18616035
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vernet,C.A., Fernandes,E.R., Gerlach,V., Shimkets,R.A.,
            Malyankar,U.M., Boldog,F.L., Zerhusen,B.D., Spytek,K.A.,
            Majumder,K., Tchernev,V.T., Padigaru,M., Patturajan,M.,
            Burgess,C.E., Gangolli,E.A., Smithson,G., Rastelli,L.,
            Macdougall,J.R., Taupier,R.J., Grosse,W.M. and Alsobrook,J.P.
  TITLE     Novel proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0181578-A 7 01-NOV-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1..1064
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      269 a    248 c    323 g    224 t
ORIGIN
```

RESULT 3
AX350382

```
Qy          Query Match         89.0%;  Score 988;  DB 6;  Length 1064;
Db          Best Local Similarity   99.5%;
            Matches  991;  Conservative   0;  Mismatches   5;  Indels   0;  Gaps   0;
```

```
Qy    115 TTTGGTAGGTCAGTGAACAAATTTCCTGATAAACAGGTCCCAAGGCCTATCTGACCTACACG 174
          |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 TCTGCCTGGTCAGTGAACAAATTTCCTGATAAACAGGTCCCAAGGCCTATCTGACCTACACG 219

Qy    175 ACTAGTGTGTGGCCTTGGGTGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 ACTAGTGTGTGGCCTTGGGTGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 279

Qy    235 GAACGCTGGAACTGCCCTGGGGTCCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 294
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 GAACGCTGGAACTGCCCTGGGAAAATGCTCTTCAGCTCTCCACCCACAACAGGCCTGAGAAGT 339

Qy    295 GCTACCAGAGACTTCCTTCATACATGCTATCAGCTCTGCTGGAGTCATGTCATGTACATCATC 354
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 GCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTGCTGGAGTCATGTCATGTACATCATC 399

Qy    355 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGGGTTCAAACAAATGGA 414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGGGTTCAAACAAATGGA 459

Qy    415 AAAACAGGAGGCCATGGCTGGAGGTTCGCAGCCACAATGTGGAATTTGGGGAA 474
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 AAAACAGGAGGCCATGGCTGGATCTGGGGAGGGCTGCAGGGACAAATGTGGAATTTGGGGAA 519

Qy    475 AGGATCTCCAAACTCTTTGTGGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATG 534
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    520 AGGATCTCCAAAACTCTTTGTGGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATG 579

Qy    535 AATCTTCACAACAACAACAGGGCCGGCGAGACTGGCAGTGAGAGGCCACCATGAAAAAGGACATGC 594
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    580 AATCTTCACAACAACAACAGGGCCGGCGAGACTGGCAGTGAGAGGCCACCATGAAAAAGGACATGC 639

Qy    595 AAAATGTCATGGCATCTCTGGGAGTGCTGCAGCATACAGACACATGCTGCTTGCTGCTGAA 654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    640 AAAATGTCATGGCATCTCTGGGAGTGCTGCAGCATACAGACACATGCTGCTTGCTGCTGAA 699

Qy    655 TTCCGGGAGATGGGGAGACTGGCGGCTCCTAAAGGCCAAGTATGACCAGGCGTCGAAAAATTGAAAATG 714
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    700 TTCCGGGAGATGGGGAGACTGGCGGCTCCTAAAGGCCAAGTATGACCAGGCGTCGAAAAATTGAAAATG 759

Qy    715 GATAAGCGCGCAGCTGAGAGCTGGGAGAACACGCCCAGGGTGCCCGCTGAGGCC 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    760 GATAAGCGCGCAGCTGAGAGCTGGGAGAACACGCCCAGGGTGCCCGCTGAGGCC 819

Qy    775 TTCCTTCCTAGCGCCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACC 834
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    820 TTCCTTCCTAGCGCCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACC 879

Qy    835 TGCAATTCAGCCTGGGCATCTATGGGCACAGAGGGTCGTGAGTGCCTACAGACAGCCAC 894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    880 TGCAATTCAGCCTGGGCATCTATGGGCACAGAGGGTCGTGAGTGCCTACAGACAGCCAC 939

Qy    895 AACACATCCAGGTGGGAGGGCCGAGTAGTCGTGGGGCCCTGTCGCACTGAGTGTGGGCTGCAG 954
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    940 AACACATCCAGGTGGGAGGGCCGAGTAGTCGTGGGGCCCTGTCGCACTGAGTGTGGGCTGCAG 999

Qy    955 GTGGAAGAGAGGAAAAACTGAGGTCATAAGGCAGCTGTAACTGCAAATTCCAGTGGTGCTGT 1014
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1000 GTGGAAGAGAGGAAAAACTGAGGTCATAAGGCAGCTGTAACTGCAAATTCCAGTGGTGCTGT 1059

Qy   1015 ACGGTCAGTGTGACCAGTGTAGGCATGTGGTGTGGCAACGTATTACTGCGCACGTCTCCCCA 1074
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1060 ACGGTCAGTGTGACCAGTGTAGGCATGTGGTGTGGCAACGTATTACTGCGCACGTCTCCCCA 1119

Qy   1075 GGCAGTGCCCAGTCCCTGGGTAAGGGCAGTGCCTGA 1110
          ||||||||||||||||||||||||||||||||||||
Db   1120 GGCAGTGCCCAGTCCCTGGGTAAGGGCAGTGCCTGA 1155
```

Left column

```
Db  724 TTCCTTCCTAGCCGCAGAGCGCGGACACTGATCTTTTTAGAGGAATCACCCAGATTACTGTACC 783
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  835 TGCAATTCCAGCCCTGGGCATCTATGGCACAGAGGGGTCGTCAGTGCCTACAGAAACAGCCAC 894

Db  784 TGCAATTCCAGCCCTGGGCATCTATGGCACAGAGGGGTCGTCAGTGCCTACAGAAACAGCCAC 843
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  895 AACACATCCAGGTGGGAGCCGACGTAGCTGTGGGGCGCCTGTGCACTGAGTGTGGGGCTGCAG 954

Db  844 AACACATCCAGGTGGGAGCCGACGTAGCTGTGGGGCGCCTGTGCACTGAGTGTGGGGCTGCAG 903
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  955 GTGGAAGAGAGGAAAAACTGAGGTCATAAGCAGCTGTGGGGCGCCTGTGCACTGAGTGTGGGGCTGT 1014

Db  904 GTGGAAGAGAGGAAAAACTGAGGTCATAAGCAGCTGTGGGGCGCCTGTGCACTGAGTGTGGGGCTGT 963
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1015 ACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGACGCAAGTATTACTGCGGCACGCGTCCCCA 1074

Db  964 ACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGACGCAAGTATTACTGCGGCACGCGTCCCCA 1023
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1075 GGCAGTGCCCAGTCCCTGGGTAAGGGCAGTGCCTGA 1110

Db 1024 GGCAGTGCCCAGTCCCTGGGTAAGGGCAGTGCCTGA 1059
```

```
RESULT 4

LOCUS       AY009402    1597 bp    mRNA    linear   PRI 13-DEC-2000
DEFINITION  Homo sapiens WNT8d precursor (WNT8d) mRNA, complete cds.
ACCESSION   AY009402
VERSION     AY009402.1  GI:11693045
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1597)
  AUTHORS   Testa,T.T., Mosakowska,D.E., Carter,P.S., Hu,E., Zhu,Y.,
            Kelsell,D.P., Murdock,P.R., Herrity,N.C., Lewis,C.J., Cross,D.A.,
            Culbert,A.A., Reith,A.D. and Barnes,M.R.
  TITLE     Molecular cloning and characterization of six novel human WNT genes
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1597)
  AUTHORS   Barnes,M.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-2000) Genomic Bioinformatics, Biotechnology and
            Genetics, Neurosciences and Renal Pharmacology, Smithkline Beecham
            Pharmaceuticals, New Frontiers Science Park (North), Third Avenue,
            Harlow, Essex CM19 5AW, UK
FEATURES             Location/Qualifiers
     source          1..1597
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /map="5q31"
     gene            1..1597
                     /gene="WNT8d"
     CDS             101..1168
                     /gene="WNT8d"
                     /codon_start=1
                     /product="WNT8d precursor"
                     /protein_id="AAG38662.1"
                     /db_xref="GI:11693046"
                     /translation="MGNLFMLWAALGICCAAFSASAWSVNNFLITGKAYLIYTTSVA
                     LGAQSGIEECKFQFAWRWNCEPNALQLSTHNRLRSATRETSFIHAISSAGVMYIITK
                     NCSMGDFENCGCDGSNNGKTGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALM
                     NLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKI
                     EMDKRQLRAGNSAEGHWVPAEAFLPSAAEAELIFLEESPDYCTCNSSLGIYGTEGREC
                     LQNSHNTSRWERSCGRLCTECGLQVEERKTEVISSSCNCKFQWCCTVKCDQCRHVSKY
                     YCARSPGSAQSLGRVWFGVYI"
     sig_peptide     101..172
                     /gene="WNT8d"
BASE COUNT     438 a    364 c    432 g    363 t
```

Right column

```
ORIGIN
Query Match  87.7%;  Score 974;  DB 9;  Length 1597;
Best Local Similarity  99.5%;  Pred. No. 5.9e-279;
Matches  977;  Conservative  0;  Mismatches  5;  Indels  0;  Gaps  0;

Qy  115 TTTGGTTAGGTCAGTGAACAATTCCTGATAAACAGTTCCCAAGGCCTATTCTGACCTACACG 174
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161 TCTTGCCTGGTCAGTGAACAATTTCCTGATAAACAGTTCCCAAGGCCTATTCTGACCTACACG 220

Qy  175 ACTAGTGTGGCCTTTGGGGTGCCCAGAGTGGCATCGAGAGAGTGCAAGTTCCAGTTTGCTTGG 234
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221 ACTAGTGTGCCCTTTGGGGTGCCCAGAGTGGCATCGAGAGAGTGCAAGTTCCAGTTTGCTTGG 280

Qy  235 GAACCGTGGAACTGCCCTGAAAATGCTCTTCCAGTCTCCACCACCACCACCAAAACAGGCTGAAGT 294
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281 GAACCGTGGAACTGCCCTGAAAATGCTCTTCCAGTCTCCACCACCACCACCAAAACAGGCTGAAGT 340

Qy  295 GCTACCAGAGAGACTTCCTTCATACATGCTATCAGTCTCTGGGAGTCATGTACATCATCATC 354
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  341 GCTACCAGAGAGACTTCCTTCATACATGCTATCAGTCTCTGGGAGTCATGTACATCATCATC 400

Qy  355 ACCAAGAAACTGTAGCATGGGGTGACTTCGAAAACTGTGGCTGTGATGGGGTCAAAACAATGGA 414
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  401 ACCAAGAAACTGTAGCATGGGGTGACTTCGAAAACTGTGGCTGTGATGGGGTCAAAACAATGGA 460

Qy  415 AAAACAGGAGCGGGCCATGGCTCTGGATCTCGGGAGGGCTCCAGCACAATGTGGAATTTGGGAA 474
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  461 AAAACAGGAGCGGGCCATGGCTCTGGATCTCGGGAGGGCTCCAGCACAATGTGGAATTTGGGAA 520

Qy  475 AGGATCTCCAAAACTCTTTGTTGGACAGTTTGGAGAAGGGGGAGGGATCCCAGAGCCCTGATG 534
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  521 AGGATCTCCAAAACTCTTTGTTGGACAGTTTGGAGAAGGGGGAGGGATCCCAGAGCCCTGATG 580

Qy  535 AATCTTCACACAACAACAGGGCCGGCAGACTGCAGTCAGTCGAGACGCCACCATGAAAAGGACATGC 594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  581 AATCTTCACACAACAACAGGGCCGGCAGACTGCAGTCAGTCGAGACGCCACCATGAAAAGGACATGC 640

Qy  595 AAAGTCATGGCCATCTCTCTGGGAGCTGCCAGCATACAGACATACGATGCTGCTTGGCTGCTGCTGAA 654
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  641 AAAGTCATGGCCATCTCTCTGGGAGCTGCCAGCATACAGACATACGATGCTGCTTGGCTGCTGCTGAA 700

Qy  655 TTCCCGGGAGATGGGAGACTACCTAAAAGGCCAAGTATGACAGGCGCGCTGAAAATTGAAATG 714
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  701 TTCCCGGGAGATGGGAGACTACCTAAAAGGCCAAGTATGACAGGCGCGCTGAAAATTGAAATG 760

Qy  715 GATAAGCGGCAGCTGAGAGCTGGGAACAGCCCGCAAGGGCCACTGGGTGCCGCTGAGGCC 774
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  761 GATAAGCGGCAGCTGAGAGCTGGGAACAGCCCGCAAGGGCCACTGGGTGCCGCTGAGGCC 820

Qy  775 TTCCTTCCTAGCGCAGCGCGGAGGCGGGAACTGAATCTTTTTTAGAGGAATCACCCAGATTACTGTACC 834
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  821 TTCCTTCCTAGCGCAGCGCGGAGGCGGGAACTGAATCTTTTTTAGAGGAATCACCCAGATTACTGTACC 880

Qy  835 TGCAATTCCAGCCCTGGGCATCTATGGCACAGAGGGTCGTCAGTGCCTACAGAAACAGCCAC 894
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  881 TGCAATTCCAGCCCTGGGCATCTATGGCACAGAGGGTCGTCAGTGCCTACAGAAACAGCCAC 940

Qy  895 AACACATCCAGGTGGGAGCCGACGTAGCTGTGGGGCGCCTGTGCACTGAGTGTGGGGCTGCAG 954
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  941 AACACATCCAGGTGGGAGCCGACGTAGCTGTGGGGCGCCTGTGCACTGAGTGTGGGGCTGCAG 1000

Qy  955 GTGGAAGAGAGGAAAAACTGAGGTCATAAGCAGCTGTTAACTGCAAATTCCAGTCTGGTGCTGT 1014
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1001 GTGGAAGAGAGGAAAAACTGAGGTCATAAGCAGCTGTTAACTGCAAATTCCAGTGGTGCTGT 1060

Qy 1015 ACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGACGCAAGTATTACTGCGGCACGCGTCCCCA 1074
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1061 ACGGTCAAGTGTGACCAGTGTAGGCATGTGGTGACGCAAGTATTACTGCGGCACGCGTCCCCA 1120

Qy 1075 GGCAGTGCCCAGTCCCTGGGTA 1096
            ||||||||||||||||||||||
Db 1121 GGCAGTGCCCAGTCCCTGGGA 1142
```

```
RESULT 5
AX153809
LOCUS       AX153809      1245 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0138353.
ACCESSION   AX153809
VERSION     AX153809.1  GI:14535436
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Holloway,J.L.
  TITLE     Human wnt gene
  JOURNAL   Patent: WO 0138353-A 1 31-MAY-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1245
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             1..>1245
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC42599.1"
                     /db_xref="GI:14535437"
                     /translation="MGNLFMLWAALGICCAAFSASAMSVNNFLITGPKAYLTYTTSVA
                     LGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATRETSFIHAISSAGVMYIITK
                     NCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALM
                     NLHNNRAGRLVVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKI
                     EMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECL
                     QNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKY
                     YCARSPQSAQSLELSVTPTNLPTWTLCQKOQEFGFLIYHRLPAKDSFQGNTASFRFVS
                     YSPISLPFWFILNKLAIIKVTEQ"
BASE COUNT      318 a     306 c     347 g     274 t
ORIGIN
```

```
Qy    Query Match      87.3%;  Score 969.4;  DB 6;  Length 1245;
      Best Local Similarity   99.4%;  Pred. No. 1.4e-277;
      Matches  973;  Conservative    0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy    115 TTTGGTAGGTCAGTGAACAAATTTCCTGATAATAACAGGTCCCAAGGCCTATCTGACCTACACG 174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTGCCTGGTCAGTGAAACAAATTTCCTGATAATAACAGGTCCCAAGGCCTATCTGACCTACACG 120

Qy    175 ACTAGTGTGGCCCTTGGGGTGCCCAGAGTGGCCATGGGAGTGCAAGTTCCAGTTTGCTTGG 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ACTAGTGTGGCCCTTGGGGTGCCCAGAGTGGCCATGGGAGTGCAAGTTCCAGTTTGCTTGG 180

Qy    235 GAACGCTGGAACTCCCCTGGGGTGCCCGAAAAATGCTCTTCAGTCTCCACCACAACAGGCTGAGAAGT 294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAACGCTGGAACTCCCCTGAAAAATGCTCTTCAGTCTCCACCACAACAGGCTGAGAAGT 240

Qy    295 GCTACCAGAGAGGACTTCCTTCATTCATAACATGCTATCACAGGCTGAGAAGT 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCTACCAGAGAGACTTCCTTCATCATCATGCTATCAGCTCTCTGCTCGAGTACATCATC 300

Qy    355 ACCAAGAACTGTAGGACTTGACTTCGAAAAACTGTTGGCTGTGTGATGGGTCAAACAAATGGA 414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACCAAGAACTGTAGGACTTGACTTCGAAAAACTGTTGATGGGTCAAACAAATGGA 360

Qy    415 AAAACAGGAGGCCATGGGACTGGATTCTGGGGAGGGCTGCAGCGACACAATGTGAAATTTGGGAA 474
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AAAACAGGAGGCCATGGCTGGATCTGGGGAGGGCTCCAGCGACAATGTGGAATTTGGGAA 420

Qy    475 AGGATCTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGATGCCAGAGCCCTGATG 534
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGATCTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGGATGCCAGAGCCCTGATG 480

Qy    535 AATCTTCACAACAACAGGGGCCGGCAGACTGGCAGTGAGAGACGCCACCATGAAAAGGACATGC 594
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AATCTTCACAACAACAGGGGCGGGCAGACTGGCAGTGAGAGGAGGCCCACCATGAAAAGGACATGC 540

Db    541 AAAATGTCATGGCATCTCTGGGAGCTGTGCAGCATACAGCATCACAGTCGCATGCTGGCTGAA 600

Db    595 AAAATGTCATGGCATCTCTGGGAGCTGTGCAGCATACAGCATCACAGTCGCATGCTGGCTGAA 654

Qy    595 TTCCCGGGAGATGGGAGACTACCTAAAGGCGCCTGCAGCCAAGTATGACCAGGCG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TTCCCGGGAGATGGGAGACTACCTAAAGGCGAAGTATGACCAGGCG 660

Qy    655 TTCCCGGGAGATGGGAGACTACCTAAAGGCGCCTGCAGCCAAGTATGACCAGGCG 714
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GATAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTG 720

Qy    715 GATAAGCGGCAGCTGAGAGCTGGGAACAGCGCCGAGGGCCACTGGGTGCCCGCTG 774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTCCTTTCCTAGGCGACACGAGGGCCGAACTGATCTTTTTGAGGAATCACCAGTT 780

Qy    775 TTCCTTTCCTAGGCGACGAGAGGGCCGAACTGATCTTTTTGAGGAATCACCAGTT 834
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGCAATTCCAGCCCTGGGCATTCTATGGCACAGAGGGTCGTGAGTGCCTACAGAA 840

Qy    835 TGCAATTCCAGCCCTGGGCATTCTATGGCACAGAGGGTCGTGAGTGCCTACAGAA 894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AACACATCCACAGGTGGGAGCCACGTAGCCTGTGGCGCCGCCTGTTCCGCACTGA 900

Qy    895 AACACATCCACAGGTGGGAGCCACGTAGCCTGTGGCGCCGCCTGTTCCGCACTGA 954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTGGGAAGAGAGGAAAAACTGAGGTCATTAAGCAGCTGTTAAACTGGCAAAATCC 960

Qy    955 GTGGGAAGAGAGGAGGAAAAACTGAGGTCATTAAGCAGCTGTTAAACTGCAAAATTCCAGTTGGT 1014
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACGGTCAAGTGTGACCAGTGTAGGCCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCCA 1020

Qy   1015 ACGGTCAAGTGTGACCAGTGTAGGCCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCCA 1074
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGCAGTGCCCAGTCCCTGG 1039

Qy   1075 GGCAGTGCCCAGTCCCTGG 1093
          |||||||||||||||||||
```

```
RESULT 6
MMWNT8DPT
LOCUS       MMWNT8DPT      1747 bp    mRNA    linear   ROD 01-JUL-1996
DEFINITION  M.musculus mRNA for wnt-8D protein.
ACCESSION   Z68889
VERSION     Z68889.1  GI:1419029
KEYWORDS    wnt-8D protein.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1747)
  AUTHORS   Bouillet,P., Oulad-Abdelghani,M., Bronner,S., Dolle,P. and
            Chambon,P.
  TITLE     Mwnt-8D: a novel mouse Wnt-8 gene induced by retinoic acid in P19
            embryonal carcinoma cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1747)
  AUTHORS   Bouillet,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-1996) Philippe Bouillet, I.G.B.M.C., 1 Rue
            Laurent Fries, Illkirch, 67404, France
FEATURES             Location/Qualifiers
     source          1..1747
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /cell_line="P19"
                     /cell_type="embryonal carcinoma"
     gene            1..1747
                     /gene="wnt-8D"
     CDS             57..1121
                     /gene="wnt-8D"
                     /codon_start=1
```

/product="wnt-8D protein"
/protein_id="CAA93117.1"
/db_xref="GI:1419030"
/db_xref="Mgi:107924"
/db_xref="SWISS-PROT:Q64527"
/translation="MGHLLMLWVAAGMCYPALGASAWSVNNFLITGPKAYLTYTASVA
LGAQIGIEECKFQFAWERWNCPEHAFQFSTHRLRATRETSFIHAIRSAAIMYAVTK
NCSMGDLENCGCDESQNGKTGHGWIWGGCSDNVEFGEKISRLFVDSLEKGDARALV
NLHNNRAGRLAVRASTKRTCKHCHGISGSCSIQTCWLQLADFRQMGNYLKAKIDRALKI
EMDKRQLRGAREGRWNALTEAPLPSTEAELIFLEGSPDYCNRNASLSIQTEGRECL
QNARSASRREQSCGRLCTECGLQVEBRAEAVSSCDGNFQWCCTVKCGQCRRVVSRY
YCTRPVGSARPRGRGKDSAW"

polyA_signal   1726..1731
/gene="wnt-8D"

BASE COUNT   409 a   436 c   531 g   371 t
ORIGIN

Query Match   Best Local Similarity   66.8%;   Score 741.6;   DB 10;   Length 1747;
84.0%;   Pred. No. 1.4e-209;
Matches 837;   Conservative   0;   Mismatches 159;   Indels   0;   Gaps   0;

```
Qy    114 TTTTGTAGGTCACTGAACAAATTTCCTGATAACAGGTCCCAAGCCCTATCTGACCTACAC 173
          ||||| ||||||||||||||| ||||||||||||  |||||||||||||||||||||||||
Db    116 TTCTGCCCTGGTCAGTGAACAAACTTCCTGATAACCGGTCCCAAGCCCTATCTGACCTACAC 175

Qy    174 GACTAGTGTGGGCCCTTGGGGTGCCCAGAGTGGCATCCAGAGAGTGCAAGTTCCAGTTTGCTTG 233
          ||| ||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||| ||
Db    176 CGGCCAGTGTGGGCCCTTGGGGTGGCTCAGAATTGCCATCCAGAAGAGTGTAAGTTCCAGTTTGCCTG 235

Qy    234 GGAACGGCTGGAACTGCCCTGAAAATGCTCTTCAGCTCTCCACCCACAACAGGCTGAGAAG 293
          |||| |||||||| |||||||  |||||||| ||||||||||||||||||||||||||
Db    236 GGAACGGGTGGAATTGTCCTGAGCATGCTTTTCAGTTTTCAACCCAACAACAGGCTGCGGAGC 295

Qy    294 TGCTACCAGAGAGACTTCCTTCATTACATCTCTTGCTGTGGAGTCATGTACATCAT 353
          ||||| ||||||||| |||||||||| ||||||||||||||||||||||||||||||
Db    296 TGCCACGAGAGAGCATCCTTCATTCCGCCTGCTGCCATCAATGTACGGCAGT 355

Qy    354 CACCAAGAACTGTAGCATGGGTGACTTGGGCTGTGTGGCTGATGGGTCAAACAAATGG 413
          |||||||||||||||||||||||| |||||| |||||||||||||||||||||||||||
Db    356 CACCAAGAACTGCAGCATGGGTGACTTGGAAAACTGCGGCTGTGACGAGTCACACAAATGG 415

Qy    414 AAAAACAGGAGGCCCATGGCCTGGATCTGGGAGGCTGCAGCACCAATGTGGAATTTGGGGA 473
          |||||||||| |||||||||  |||||||||||||||||||||||||||  |||||||||||
Db    416 AAAAACAGGTGGCCCATGGGCTGGAATCTGCAGGCTGCAGCGGACACAACGTGGAGTTCGGGGA 475

Qy    474 AAGGATCTCCAAACTCTTTGTGGACAGTTTGGCGGAGGGGGGAAGATGCCAGAGCGTTCAGA 533
          ||| ||||| || |||||| ||| ||||| |||||||||||||||||||||| ||||||||||
Db    476 AAAAATCTCCAGACTCTTCGTGGACAGTTTGGAGAAAAGGACAGAGCCCTGGT 535

Qy    534 GAATCTTCACAACAACAGGCGCGGCCGAGACTGGACCGTGAGAGCCAGCAGCACATG 593
          |||| |||||||||||||||||||| ||||||||||  |||||||||||||| ||||
Db    536 GAACCTTCACAACAACAGGGCCGCGAGACTGGACCGTGAGGGGTCCACGAAAAGGACCTG 595

Qy    594 CAAATGTCATGGCATCTCTGGGAGTGCAGCATCAGACAATGCTGGCTGGCTGGCTGA 653
          |||||||||||||||||||||  |||||||||||||||||| |||||||||||||||||
Db    596 CAAGTGTCATGGCCATCTCAGGGAGTGCAGCACCATCCAGCATGGCTGGCTGA 655

Qy    654 ATTCCGGGAGATGGGGAGCTTACTTAAAGGCCCAAGTATATGACCGGCTGAAAAATTGAAAT 713
          |||||| |||||||| |||| |||||||||||||||||||||| |||||||||  ||||||||
Db    656 CTTCCGGCAGATGGGAAATATACCTAAAGGCTGAAGTTCTCGACTACTGCAA 715

Qy    714 GGATAAGCGGCAGCTGGGAACAGCTGGGACTGATCTTTTAGAGGAATCACCAGATTACTGTAC 773
          |||| |||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Db    716 GGACAAGCGCCAGCTAAGGGGCTGCAGAGCCGGCTGGGCTCTCACGGAGGC 775

Qy    774 CTTCCTTCCTGAGGCGGAGGAATCACCACAGATTACTGTAC 833
          ||||||||||||||||||||||||| |||||||||||||||
Db    776 CTTCCTTCCCAGCCACAGAGGCTGATCTTCCTGGAACTACTGCAA 835

Qy    834 CTGCAATTCCAGCCTGGGCATCTATGGACAGAGAGGGGTCTTGAGTGCCTACAGAAGACAGCCCA 893
          ||||||  ||||||||||||||||||| ||| || |||||||||||||||||||||| ||||||||
Db    836 CCGCAACGCGCCAGCTTGAGCATTCAGACGGAATGCCCGGGGGAGCGGGAGTGCCTGCAGAATGCCCG 895
```

RESULT 7

LOCUS   AX153811   1245 bp   DNA   linear   PAT 22-JUN-2001
DEFINITION   Sequence 3 from Patent WO0118353.
ACCESSION   AX153811
VERSION   AX153811.1   GI:14535438
KEYWORDS   .
SOURCE   synthetic construct
   ORGANISM   synthetic construct
     artificial sequences.
REFERENCE   1   (bases 1 to 1245)
   AUTHORS   Holloway,J.L.
   TITLE   Human wnt gene
   JOURNAL   Patent: WO 0118353-A 3 31-MAY-2001;
     ZymoGenetics, Inc. (US)
FEATURES   Location/Qualifiers
   source   1..1245
     /organism="synthetic construct"
     /mol_type="genomic DNA"
     /db_xref="taxon:32630"
     /note="This degenerate sequence encodes the amino acid
     sequence of SEQ ID NO:2."

BASE COUNT   214 a   105 c   230 g   167 t   529 others
ORIGIN

Query Match   Best Local Similarity   63.8%;   Score 708.4;   DB 6;   Length 1245;
56.5%;   Pred. No. 1.1e-199;
Matches 564;   Conservative   258;   Mismatches 176;   Indels   0;   Gaps   0;

```
Qy     96 CTGCCTCCACTTTTCTCTTTTGGTTTTGGTAGGTCAGTGAACAAATTTCCTGATAACAGGTTCCCAA 155
          |:|:| ::|| ||| ||::|| |||| :||:|| ||||||||||||||||| |||||||||||||
Db     42 YTGYGYGCNGTGYYCNTTYWSNGCNTGGWSNGCNTGGWSNGTNAAYAAYTTYYTNATHACNGGNCCNAA 101

Qy    156 GGCCTATCTGACCTACACGACTAGTGTGGGCCCTTGGGGTGCCCAGAGTGGCATCGAGAGTG 215
          |||:| | ||||||:||:||:| :|:|| ||| ||||| |||:|||| :||||| ||:|||
Db    102 RGCNTAYYTNACNTAYACNGCNWSNGTNGGNCNYTNGGNGCNCARWSNGGNATHGARGARTG 161

Qy    216 CAAGTTCCAGTTTGCTTGGGAAAACGGTGGAACTGCCCTGAAAATGCTCTTCTTCCAC 275
          ||| ||||| |||||:|||||:||: :| |||| |||| |||||||||| |:| |:| |
Db    162 YAARTTYCARTTYGCNTGGGARMGNTGGAAYTGYCCNGARAAYGCNYTNCARYTNWSNAC 221

Qy    276 CCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTGC 335
          ||:|| ||||:||||| |||:|::||||||:| ||::| ||:||:|::| |||:|:|:|||
Db    222 NCAYAAYAMYGNYTNMGNWSNGCNACNMGNGARACNMSNTTYATHCAYGCNATHWSNWSNGC 281

Qy    336 TGGAGTCATGTACATCACCAAGAACTGTAGCATGGGTGACTTGAAAAACTGTGGCTG 395
          |||| ||||:|| |||:| |||||:|| :| |||||:|| |:| :|||:|||:|||:|
Db    282 NGGNGTNATGTAYATHACNAARAAYTGYWSNATGGGNGAYTTYGARAARYTGYGGNTG 341

Qy    396 TGATGGGTCAAACACATTGGGAAAAAACAGGAGGCCCATGGCCTGGATCTGGGAGGCGA 455
          |||:||::|:||:|| |:|||:|:||:||||:|||||:||| |||||:|||||:|| :| 
Db    342 YGAYGGNWSNAAYAYAYGNARACNNGGNGGNCCNATHGGNTGGATHTGGGGNGGNGA 401

Qy    456 CAATGTGGGAATTTGGGGAAAGGATCTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGGAA 515
          ||| |:|| || | ||||:||:||:|||||:|||: |:| |||:|| | | |||:|:|:|| 
Db    402 YAAYGTNGGNARTTYGNGARMGNATHWSNAARYTNTNGTNGAYAGYWSNYTNGARAARGGNAA 461
```

```
Qy    954 GGTGGAAGAGAGGGAAAACTGAGCCAGCGCAGGCGCAGCTGTTTTGGGGGGCGGGGCTGCA 1013
          |||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db    896 GGTGGAGGAGGAGGACAGAGCCCTGGTCAATCTGCACAACAACAGGGCCGCGAGACTGGACCGTGAGG 955

Qy   1014 TACGGTCAAGTGTCAGACCAGGTTAGGCCATGTGGTCAAGTATTACTGCGGCACGGCTCCC 1073
          |:||| ||| |||||  ||||||||||| ||:||||| ||:|:|::|||| |:||||| :||
Db   1016 CACTGTCAAGTGTCAGCATTCAGACGGAATGCCCGGGGGAGCGGGAGTGCCTGCAGAATGCCCG 1075

Qy   1074 AGGCAGTGCCCAGTTCCCTGGGTAAGGGCAGTGCCTG 1109
          |||||||||||||| |||||||||||| |||||||||
Db   1076 AGGTAGTGCCCAGGCCCCGGGCCCCGGGCCAGGGGCCAAGGACAG 1111
```

```
RESULT 8
GGU02097
LOCUS       GGU02097      1734 bp    mRNA      linear   VRT 11-JUN-1994
DEFINITION  Gallus gallus white leghorn Wnt-8C (cwnt-8C) mRNA, complete cds.
ACCESSION   U02097
VERSION     U02097.1  GI:403577
KEYWORDS    .
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1734)
  AUTHORS   Hume,C.R. and Dodd,J.
  TITLE     Cwnt-8C: a novel Wnt gene with a potential role in primitive streak
            formation and hindbrain organization
  JOURNAL   Development 119 (4), 1147-1160 (1993)
   MEDLINE   94139958
    PUBMED   7916678
REFERENCE   2  (bases 1 to 1734)
  AUTHORS   Hume,C.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-1993) Clifford R Hume, Physiology and Cellular
            Biophysics, Columbia University, College of Physicians and
            Surgeons, 630 W. 168 St., New York, NY 10032 USA
FEATURES             Location/Qualifiers
     source          1..1734
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="white leghorn"
                     /db_xref="taxon:9031"
     gene            1..1734
                     /gene="cwnt-8C"
     CDS             89..1162
                     /gene="cwnt-8C"
                     /codon_start=1
                     /product="Wnt-8C"
                     /protein_id="AAA18933.1"
                     /db_xref="GI:403578"
                     /translation="MRGSTFLLLSIVGIYGAILNAAWSVNNFLMTGPKAYLTYSSSV
                     AAGAQSGMEECKFQFGWERWNCPBSALQLSTHNRLRSATRETSFVHAISSAGVWYTLT
                     RNCSLGDFESCCGCDDSRNGRVGRGWVWGGCSDNVEFGERISKLLFVDALETGHDTRAL
                     INLHNNEVGRLAVKATMKRACKCHGVSGSCSIQTCWLQLADFREIGNYLKMKYDQAHK
                     LEMDKRRMRAGNSADSRGATAETFPHHVHSTELVPFLEDSPDYCTRNASLGHHGTEGREC
                     LQTGKNLSQWERRSCRRLSTECGLKVEERRTEVVSSCNCKFHWCCTVRCEQCRQLVAK
                     HFCARRDAAVANHTKRRNKGHRR"
ORIGIN
BASE COUNT   387 a    460 c    526 g    361 t
```

```
Query Match.          51.3%;   Score 569.4;   DB 5;   Length 1734;
Best Local Similarity  75.1%;    Pred. No. 3.4e-158;
Matches  711;   Conservative   0;  Mismatches 236;   Indels   0;   Gaps   0;

Qy    122 GGTCAGTGAACAATTCCTGATAACAGGTGCCTAAGCGTTCCCAAGGCCTATCTGACCTACACGACTAGTG 181
          |||||  |  ||| ||  || || || || | |  ||||  || || ||||||| || || ||| |||||
Db    159 GGTCGGTGAATTAACTTTCTGATGACAGGAACCTAAGGCGTACGGAGCCGACGTACCTGACGACCTAGTG 218

Qy    182 TGGCCTTGGGGTGCCCAGAGTGGGCATCGAGGAGAGTGCCAGAGTTCCAGTTTGCTTGGGAAGGCT 241
          |||| || || ||  ||||||| ||||| || || ||| |||| ||  ||||| ||||| ||||||
Db    219 TGGCCGCGGGCGCGCACAGAGTGGGCATCGAGGACGGAGTGCCAGGTTCCAGTTCGGAGTGGGGAGGGCT 278

Qy    242 GGAACTGCCCTGAAAATGCTCTTCAGCTCTATCAGCTGCTGTTGTGTCAGTGCATACATCACCAAGA 301
          |||| || ||| |   ||  ||  || || ||  || || || || || || || |||||||| |||
Db    279 GGAACTGCCCCGAGACGTGCCGCATCCAGTCGCCCTGGGTTGTTACAACCTGACCAGTGCTACCA 338

Qy    302 GAGAGACTTCCTTCAATACATGCTATCAGCTTGCTTGGTGAAGTGCTACCA 361
          |||||| || ||| || || ||  ||||| ||||| || |||||||||||
Db    339 GAGAGACATCCTTTGTGCACGCCATCAGCTTCCGCTGGTGTTATGTACACCCTGACCAGGA 398

Qy    362 ACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGGTCAAAACAATGGAAAAACAG 421
          ||||| || ||||| |||||||||||||| |||| || ||||| |||||| ||||||
Db    399 ACTGCAGCTTAGGAGACTTCGAGAGCTGCTGCGGCTGTGATGACTCCAGGAACGGGCGTGTAG 458

Qy    422 GAGGCCATGGCCTGATCTGGGGAGGCTGCAGCGCGACAGATGTGGAATTTGGGGAAAGGAAATCT 481
          |||| |||| || || || ||||| |||| ||  | ||  || |||||| |||| ||||| |
Db    459 GTGGCCGAGGCTGGGTTCTGGGGAGGCTGCAGCGATAACGTGGAGTTTGGGGAGAGGATT 518

Qy    482 CCAAACTCTTTGTGGAACAGTTTGGAGAAGGGAAGGATGGCCAGAGCGCCCTTCGGATCTTC 541
          || |||||||| |||| ||||| ||||  |||||||| || ||  ||||||| ||||||| ||
Db    519 CCAAGCTCTTTGTGGATGCTTTGGAAACGGGACATGACACCCGTGCCCTGATCAACCTGC 578

Qy    542 ACAACAACACGGGCCCGGCCAGACTGGCAGTGAAGGCAACATGCAAGTC 601
          ||||| |||| ||| |  || |||||| || || ||  ||||| |||||
Db    579 ACAACAACGAAGTCGGGGAGACTTGGCAGTGAAAGCCACAATGAAGCGAGCCTGC 638

Qy    602 ATGGCCATCTCTGGGAGCTGCGCATACACAGACATGTGGCTGCAGCTGGCAGATTTCCGGG 661
          ||||| ||||| || ||| |||| ||||  ||||| || |||| |||  |||||| |||||
Db    639 ATGGGGTGTCAGGCAGTTGCAGCATCCAGACAACGTGCTGGCTGCAGCTGGCAGACTTCGGG 698

Qy    662 AGATCGGGAGACTACCTAAGGCCAAGTATGACCAGGCGCTGAAAAATTGAAATGGATAAGC 721
          ||||| || |||| || |||||| || || ||||| || ||  | |||||||||| || ||
Db    699 AGATTGGCAACTACCTGAAGATGAAATACGACCAGGCTCATAAGCTGGAGATGGACAAGA 758

Qy    722 GGCAGGCTGAGGAGCTGGGAACAGCGCCGAGGGGCCACTGGGGTCGCCCGCTGAGGCTTC 781
          |||| ||| |  || ||||||| | | ||||||| ||||| || || |||| |||||  |
Db    759 GGCGGATGAGAGCTGGCAGCAGCGCCCACTGAGTCCCGCCTCTGAGCCGCTGAGGCTTCCACC 818

Qy    782 CTAGCGCAGAGGCGCGAAACTGAATCATCTTTTTTACAGGAATCACAGGATTACTGTACCTGCAATT 841
          |||||| ||| | || |  ||||  |||  || || ||||| |  || ||||||||  | || || |
Db    819 ACGTCCACTCCACGGAGCTGCGTCTTCTTTGGAGGACTCCACGAGGAAACG 878
```

RESULT 9

```
Qy    842 CCAGCCTGGGCCATCTTATGGCACAGAGGGTCGTGAGTGCCTTACAGAACAGCCACACAT 901
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    879 CCAGCCTGGGCCACCACAGAGGGCACCAGAGGGCCCGAGTGCCTTACAGAACAGCCACACAT 938

Qy    902 CCAGGTGGGAGCGACGTAGCTAGTGTGGGGCGCTGCGCTGTGTGGGGCTGCAGGTGGGAAG 961
          |||||| ||||||||| |||||| ||||||||||||||||| |||||||||||||||||||
Db    939 CTCAGTGGGAGCGACGGAGGAGCGTGCCCGCGGGCTCTCGACACGGAGTGCGCGCCTCAAAGTGGGAGG 998

Qy    962 AGAGGAAAACTGAGGTCATAAGCAACTGTRAACTGCGCAAAATTCCAGTGGTGGTTGCTGGGTTACGGTCA 1021
          ||||| |||||||||| |||| ||| |||||||||||||||||||||||||||||||||||
Db    999 AGAGGAAGACAGAGGTGGTTCGAGCAACTGCCAACTGCGCAAGTTCCACTGGTGGTTGCTGCACGGGTG 1058

Qy   1022 AGTGTGACCAGTGTAGGCATGTGGGTTGCAGAAGTATTTACTCCGCACGC 1068
          ||| | |||||||||||||||||||||||||||||||||||||||| |||
Db   1059 GGTGCGGAGCAGTGCCCGGGCCAGCTGGTGGCCAAGCACTTCGTGCCCGC 1105
```

LOCUS   AC004826   149172 bp   DNA   linear   PRI 07-OCT-2000
DEFINITION   Homo sapiens PAC clone RP1-309D19 from 5, complete sequence.
ACCESSION   AC004826
VERSION   AC004826.3   GI:7767904
KEYWORDS   HTG.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 149172)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE   Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2 (bases 1 to 149172)
  AUTHORS   Ozersky,P., Goela,D., Edwards,J. and Harper,M.
  TITLE   The sequence of Homo sapiens PAC clone RP1-309D19
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 149172)
  AUTHORS   Waterston,R.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4 (bases 1 to 149172)
  AUTHORS   Waterston,R.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (10-MAY-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5 (bases 1 to 149172)
  AUTHORS   Waterston,R.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-JUN-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6 (bases 1 to 149172)
  AUTHORS   Waterston,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (07-OCT-2000) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
  COMMENT   On May 10, 2000 this sequence version replaced gi:7630755.
            -------------------- Genome Center
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site: http://genome.wustl.edu/gsc
            Contact: sapiens@watson.wustl.edu
            -------------------- Summary Statistics
            Center project name: H_DJ0309D19

            NOTICE: This sequence may not represent the entire insert of this
            clone. It may be shorter because we only sequence overlapping

            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO. For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            This clone was derived from human PAC library RPCI-1, prepared by
            Pieter de Jong and coworkers at the Roswell Park Cancer Institute
            (http://bacpac.med.buffalo.edu) using the method described by
            Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
            one male donor.
            The clone may be obtained either from Genome Systems, Inc.
            (http://www.genomesystems.com) or Research Genetics, Inc.
            (http://www.resgen.com); or from Pieter de Jong.
            VECTOR: pCYPAC2
            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-505H15. Actual start of
            this clone is at base position 1 of RP1-309D19; actual end is at
            base position 149172 of RP1-309D19.
FEATURES   Location/Qualifiers
    source   1..149172
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="5"
            /map="5"
            /clone="RP1-309D19"
            /clone_lib="RPCI-1"
    repeat_region   1..254
            /rpt_family="Alu"
    repeat_region   258..415
            /rpt_family="L1"
    repeat_region   404..501
            /rpt_family="L1"
    repeat_region   557..842
            /rpt_family="Alu"
    repeat_region   876..1002
            /rpt_family="Alu"
    repeat_region   1116..1457
            /rpt_family="Alu"
    repeat_region   3009..3106
            /rpt_family="MER81"
    repeat_region   3110..3226
            /rpt_family="MIR"
    repeat_region   3463..3502
            /rpt_family="L2"
    repeat_region   3613..3754
            /rpt_family="MER1_type"
    repeat_region   3775..4077
            /rpt_family="MER1_type"
    repeat_region   4477..4778
            /rpt_family="Alu"
    misc_feature   4894..4906
            /note="match to EST AA224756 (NID:g1846150) nc33c09.s1"
    repeat_region   4908..5024
            /rpt_family="Alu"
    repeat_region   5048..5203
            /rpt_family="Alu"
    repeat_region   5206..5324
            /rpt_family="MIR"
    repeat_region   5400..5686

```
repeat_region   6735..7032
                /rpt_family="Alu"
repeat_region   7036..7341
                /rpt_family="Alu"
repeat_region   7438..7741
                /rpt_family="Alu"
repeat_region   9199..9267
                /rpt_family="Alu"
repeat_region   9372..9670
                /rpt_family="MIR"
repeat_region   10024..10313
                /rpt_family="Alu"
repeat_region   10645..10932
                /rpt_family="Alu"
repeat_region   11059..11177
                /rpt_family="Alu"
repeat_region   11191..11511
                /rpt_family="Alu"
repeat_region   11514..11809
                /rpt_family="Alu"
repeat_region   11811..12117
                /rpt_family="Alu"
repeat_region   12796..13091
                /rpt_family="Alu"
repeat_region   13668..13771
                /rpt_family="MIR"
repeat_region   14110..14397
                /rpt_family="MIR"
repeat_region   14706..14883
                /rpt_family="Alu"
repeat_region   1599..19601
                /rpt_family="Alu"
repeat_region   15660..15719
                /rpt_family="MER1_type"
repeat_region   16065..16292
                /rpt_family="MIR"
misc_feature    16588..17484
                /note="similar to
                EST AW663893 (NID:g7456432) hi73c01.x1"
repeat_region   18692..18798
                /rpt_family="Alu"
repeat_region   18818..19120
                /rpt_family="Alu"
repeat_region   21117..21424
                /rpt_family="MIR"
repeat_region   22089..22391
                /rpt_family="Alu"
repeat_region   22538..22549
                /rpt_family="Alu"
repeat_region   22550..22837
                /rpt_family="Alu"
repeat_region   22838..22990
                /rpt_family="Alu"
repeat_region   23192..23491
                /rpt_family="Alu"
repeat_region   23492..23660
                /rpt_family="Alu"
repeat_region   23791..24100
                /rpt_family="Alu"
repeat_region   24288..24375
                /rpt_family="Alu"
repeat_region   24848..25136
                /rpt_family="L2"
repeat_region   25503..25460
                /rpt_family="Alu"
repeat_region   25490..25665
                /rpt_family="Alu"
repeat_region   25666..25957
                /rpt_family="L2"
repeat_region   25958..26147
                /rpt_family="L2"
```

```
Query Match   49.3%;  Score 547;  DB 9;  Length 149172;
Best Local Similarity 100.0%;  Pred. No. 2.4e-151;
Matches 547;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      564 GGCAGTGAGGAGCCACCCATGAAAAGGACACATGAAAAGTCATGGCATCTCTGGGAGCTGCAG  623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    14964 GGCAGTGAGGAGCCACCCATGAAAAGGACACATGAAAAGTCATGGCATCTCTGGGAGCTGCAG  15023

Qy      624 CATACAGACATGCTCGGCCTGCAGCTGGCTGAATTCGGGAGAGATGGGAGACTACCTAAAGGC  683
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15024 CATACAGACATGCTCGGCCTGCAGCTGGCTGAATTCGGGAGAGATGGGAGACTACCTAAAGGC  15083

Qy      684 CAAGTATGACCAGGCGCCTGAAAAATTGAAAATGGATAAAGCGGGCAGCTGAGAGCTGGGAACAG  743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15084 CAAGTATGACCAGGCGCCTGAAAAATTGAAAATGGATAAAGCGGGCAGCTGAGAGCTGGGAACAG  15143

Qy      744 CGCCGAGGGCCCACTCGGGGTGCCCGCTGAGGGCCTTCCTTCCTTCCTTAGCCGCAGAGGGGGAACTGAT  803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15144 CGCCGAGGGCCCACTGGGGTGCCCGCTGAGGGCCTTCCTTCCTTCCTTAGCCGCAGAGGGGGGGACTGAT  15203

Qy      804 CTTTTTAGAGGAAATCACCCAGATTACTGTACCTGCAATTCAGCCTGGGCATCTATGGCAC  863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15204 CTTTTTAGAGGAAATCACCCAGATTACTGTACCTGCAATTCAGCCTGGGCATCTATGGCAC  15263

Qy      864 AGAGGGTCGTGAGTCGCCTACAGAACAGCCACAACACATCCAGGTGGGACGTGGGGACGTG  923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15264 AGAGGGTCGTGAGTCGCCTACAGAACAGCCACAACACATCCAGGTGGGACGTGGGGACGTG  15323

Qy      924 TGGGCGGCCCTGTGCACTGAGTGTGGGCTGCAGGTGGGAAGAGAGGAAAACTGAGGTCATAAG  983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15324 TGGGCGGCCCTGTGCACTGAGTGTGGGCTGCAGGTGGGAAGAGAGGAAAACTGAGGTCATAAG  15383

Qy      984 CAGCTGTAACTGCAAAATTCCAGTGGTTGCTGTACGGTTCACGGTGACCAGTGTAGGCATGT  1043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15384 CAGCTGTAACTGCAAAATTCCAGTGGTTGCTGTACGGTTCACGGTGACCAGTGTAGGCATGT  15443

Qy     1044 GGTGAGCAAGTATTACTGCGCAGCGCTCCCCAGGCACGTGCCCAGTCCCTGGGTAAGGGCAG  1103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15444 GGTGAGCAAGTATTACTGCGCAGCGCTCCCCAGGCACGTGCCCAGTCCCTGGGTAAGGGCAG  15503

Qy     1104 TGCCTGA  1110
            |||||||
Db    15504 TGCCTGA  15510


RESULT 10
AC113382/c
LOCUS       AC113382              166870 bp    DNA     linear   PRI 28-JAN-2003
DEFINITION  Homo sapiens chromosome 5 clone RP11-325L7, complete sequence.
ACCESSION   AC113382
VERSION     AC113382.2  GI:27923635
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 166870)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 166870)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 166870)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jan 28, 2003 this sequence version replaced gi:19033496.
            Draft Sequence Produced by DOE Joint Genome Institute
```

```
                 www.jgi.doe.gov
                 Finishing Completed at Stanford Human Genome Center
                 www-shgc.stanford.edu
                 Quality: Phrap Quality >=40 99.8% of Sequence;
                 Estimated Total Number of Errors is 0.2.

FEATURES         Location/Qualifiers
     source      1..16870
                 /organism="Homo sapiens"
                 /mol_type="genomic DNA"
                 /db_xref="taxon:9606"
                 /clone="RP11-325L7"
                 /chromosome="5"
BASE COUNT       45266 a    34761 c    37074 g    49769 t
ORIGIN

Query Match    49.3%;  Score 547;  DB 9;  Length 168870;
Best Local Similarity   100.0%;  Pred. No. 2.4e-151;
Matches 547;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    564 GGCAGTGAGGAGCCACCATGAGAAAAGACATGCAAAATGTCATGGACATTCTCTGGGAGCTGCAG 623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80777 GGCAGTGAGGAGCCACCATGAGAAAAGACATGCAAAATGTCATGGACATTCTCTGGGAGCTGCAG 80718

Qy    624 CATACAGACAGCATGCTGGCTGGCCGAGCTGGCTGGGAGAGTGGGAGGACTACCTAAAGGC 683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80717 CATACAGACAGCATGCTGGCTGGCCGAGCTGGCTGGGAGAGTGGGAGGACTACCTAAAGGC 80658

Qy    684 CAAGTATGACCAGGCGGCTGAAAAATTGAAATTGGATAAGCGCCAGCTGAGCAGCTGGGAACAG 743
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80657 CAAGTATGACCAGGCGGCTGAAAAATTGAAATTGGATAAGCGCCAGCTGAGCAGCTGGGAACAG 80598

Qy    744 CGCCCAGGGGCCACTCGGGTGCCCGGTGAGGGCCTTCCTTCCTTCTTCGCGAGGCGGGAACTGAT 803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80597 CGCCCAGGGGCCACTCGGGTGCCCGGTGAGGGCCTTCCTTCCTTCTTCGCGAGGCGGGAACTGAT 80538

Qy    804 CTTTTTAGGAGGAATCACCAGATTACTGTACCTGCAAATTCCAGCCTGGGCATCCTATGGCAC 863
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80537 CTTTTTAGGAGGAATCACCAGATTACTGTACCTGCAAATTCCAGCCTGGGCATCCTATGGCAC 80478

Qy    864 AGAGGGTCGTGAGTGCCTACAGAACAGCACAACACATCCAGGTGTGGGAGGACGTAGCTG 923
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80477 AGAGGGTCGTGAGTGCCTACAGAACAGCACAACACATCCAGGTGTGGGAGGACGTAGCTG 80418

Qy    924 TGGGCGGCCTTGTGCACTGAGTGTGGCGTGGGCTGAAGAGAGGAGAGAAAAACTTGAGGTTCATAAG 983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80417 TGGGCGGCCTTGTGCACTGAGTGTGGCGTGGGCTGAAGAGAGGAGAGAAAAACTTGAGGTTCATAAG 80358

Qy    984 CAGCTGTAACTGCAAATTCCAGTGGTGGTGTCTGTTACGGTCAAGTGTGACCAGTGTAGGCATGT 1043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80357 CAGCTGTAACTGCAAATTCCAGTGGTGGTGTCTGTTACGGTCAAGTGTGACCAGTGTAGGCATGT 80298

Qy   1044 GGTGAGCAAGTATTACTGGCCACACGTCCCCAGGCAGCAGTGCCCAGTCTCCCTGGGTAAGGGCAG 1103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  80297 GGTGAGCAAGTATTACTGGCCACACGTCCCCAGGCAGCAGTGCCCAGTCTCCCTGGGTAAGGGCAG 80238

Qy   1104 TGCCTGA 1110
          |||||||
Db  80237 TGCCTGA 80231
```

```
REFERENCE   1 (bases 1 to 217608)
ORGANISM    Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.
SOURCE      Pan troglodytes (chimpanzee)
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
VERSION     AC144871.1  GI:31044284
ACCESSION   AC144871
DEFINITION  Pan troglodytes clone CH251-295L2, WORKING DRAFT SEQUENCE, 14
            unordered pieces.
LOCUS       AC144871    217608 bp    DNA    linear    HTG    23-MAY-2003
RESULT 11
```

```
AUTHORS     Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K.,
            Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X.,
            Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,S.-L., Hu,P.,
            Hurle,B., Idol,J.R., Karling,E., Kwong,P., Laric,P., Lee-Lin,S.-Q.,
            Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
            Maskeri,B., McDowell,J., Paguirigan,C., Pearson,N., Portnoy,M.E.,
            Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
            Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
            Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
            NISC Comparative Sequencing Initiative
```

```
TITLE       Unpublished
JOURNAL
REFERENCE   2 (bases 1 to 217608)
AUTHORS     Green,E.D.
TITLE       Direct Submission
JOURNAL     Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     --------------- Genome Center
            Center: NIH Intramural Sequencing Center
            Center code: NISC
            Web site: http://www.nisc.nih.gov
            Contact: nisc_zoo@nhgri.nih.gov
            --------------- Project Information
            Center project name: esp
            Center clone name: 295L02
            --------------- Summary Statistics
            Sequencing vector: plasmid; n/a; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 212339 bases at least Q40
            Consensus quality: 213196 bases at least Q30
            Consensus quality: 213732 bases at least Q20
            Insert size: 181000; agarose-fp
            Insert size: 216308; sum-of-contigs
            Quality coverage: 11.33x in Q20 bases; agarose-fp
            Quality coverage: 9.48x in Q20 bases; sum-of-contigs
            ---------------.
            NOTE: This is a 'working draft' sequence. It currently
            consists of 14 contigs. The true order of the pieces
            is not known and their order in this sequence record is
            arbitrary. Gaps between the contigs are represented as
            runs of N, but the exact sizes of the gaps are unknown.
            This record will be updated with the finished sequence
            as soon as it is available and the accession number will
            be preserved.
            *        1:   2393: contig of 2393 bp in length
            *     2393:   2493: gap of unknown length
            *     2394:   5024: contig of 2531 bp in length
            *     5024:   5124: gap of unknown length
            *     5025:   7912: contig of 2788 bp in length
            *     7912:   8012: gap of unknown length
            *     7913:  11717: contig of 3705 bp in length
            *    11717:  11817: gap of unknown length
            *    11718:  20663: contig of 8846 bp in length
            *    20663:  20763: gap of unknown length
            *    20664:  33391: contig of 12628 bp in length
            *    33391:  33491: gap of unknown length
            *    33392:  44843: contig of 11352 bp in length
            *    44843:  44943: gap of unknown length
            *    44844:  55780: contig of 10837 bp in length
            *    55780:  55880: gap of unknown length
            *    55781:  72544: contig of 16664 bp in length
            *    72544:  72644: gap of unknown length
            *    72645:  88201: contig of 15557 bp in length
            *    88201:  88301: gap of unknown length
            *    88202: 105480: contig of 17179 bp in length
            *   105480: 105580: gap of unknown length
            *   105481: 141858: contig of 36278 bp in length
            *   141858: 141958: gap of unknown length
            *   141959: 179548: contig of 37590 bp in length
            *   179548: 179648: gap of unknown length
            *   179649: 217608: contig of 37960 bp in length.
FEATURES    Location/Qualifiers
```

```
source          1. 217608
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /clone="CH251-295L2"
                /clone_lib="CH251"
misc_feature    1. 2393
                /note="assembly_fragment"
misc_feature    2494. .5024
                /note="assembly_fragment"
misc_feature    5125. .7912
                /note="assembly_fragment"
misc_feature    8013. .11717
                /note="assembly_fragment"
misc_feature    11818. .20663
                /note="assembly_fragment"
misc_feature    20764. .33391
                /note="assembly_fragment"
misc_feature    33492. .44843
                /note="assembly_fragment"
misc_feature    44944. .55780
                /note="assembly_fragment"
                /vector_side:right"
                clone_end:SP6
misc_feature    55881. .72544
                /note="assembly_fragment"
misc_feature    72645. .88201
                /note="assembly_fragment"
misc_feature    88302. .105480
                /note="assembly_fragment"
misc_feature    105581. .141858
                /note="assembly_fragment"
misc_feature    141959. .179548
                /note="assembly_fragment"
misc_feature    179649. .217608
                /note="assembly_fragment"

BASE COUNT      60290 a      47208 c      47882 g      60726 t      1502 others
ORIGIN

Query Match     48.8%;  Score 542.2;  DB 2;  Length 217608;
Best Local Similarity  99.5%;  Pred. No. 6.7e-150;
Matches 544;  Conservative  0;  Mismatches  3;  Indels  0;  Gaps  0;

Qy      564 GGCAGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAG 623
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173173 GGCAGTGAGAGCCACCATGAAAAGGACATGCAAATGTCATGGCATCTCTGGGAGCTGCAG 173232

Qy      624 CATACAGACATGCTGGCTGGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGC 683
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173233 CATACAGACATGCTGGCTGGCTGGCTGAATTCCGGGAGATGGGAGACTACCTAAAGGC 173292

Qy      684 CAAGTAGTACCAGCCGCCTGAAAAATTGAAATGGATAAGCCGGCAGCTGGGAACAG 743
            ||||||| ||||||| |||||| |||||||||||||||||||||||||||||||||
Db   173293 CAAGTATGACCAGCCACTGAAAATTGAAATGGATAAGCCGGCAGCTGGGAACAG 173352

Qy      744 CGCCGAGGGCCCACTGGGGTGCCCCGCTGAGCCGCCTTCCTTCCTTAGCCGAGAGGCGGAACTGAT 803
            |||||||||||||||||||||||||||||||||||
Db   173353 CGCCGAGGGCCCACTGGGGTGCCCCGCTGAGCCGCC 173412

Qy      804 CTTTTTAGAGGAATCACCAGATTACCTGTAGCTGCAATTCACCAGAATTCCAGCCTGGGGCATCTATGGCAC 863
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   173413 CTTTTTAGAGGAATCACCAGATTACCTGTAGCTGCAATTCACCAGAATTCCAGCCTGGGGCATCTATGGCAC 173472

Qy      864 AGAGGGTCGTGAGTCCTACAGAACAGCCACACACACTGTTGTAGCTGCAGCTGAGCTG 923
            |||||||||||||||||||||||||||||||||||
Db   173473 AGAGGGTCGTGAGTCCTACAGAACAGCCACACACATCCAGGTGGGAGGACGACGTAGCTG 173532

Qy      924 TGGGCGGCCTGTGCACTGACTGTGGGCGCTGCAGGTGGGAAGAGAGGAAAAACTGAGTGTAGGA 983
            ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   173533 TGGGCGGCCTGTGCACTGACTGTGGGCTGCAGGTGGGAAGAGAGAGGAAAAACTGAGGTGTCATAAG 173592

Qy      984 CAGCTGTAACTGCAAATTCCAGTGGTGGTCGTCTACGGTCAAGTGTGACCAGTGTAGGCATGT 1043
            ||||||||||||||||||||||||||||||||||||||||||
Db   173593 CAGCGTAACTGCAAATTCCAGTGGTGGTCGTCTACGGTCAAGTGTGACCAGTGTAGGCATGT 173652

Qy     1044 GGTGAGCAAGTATATTACTGGGCACACCCTCCCCAGGCAGAGTGCCGCAGTTCCCTTAAGGGCAG 1103
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   173653 GGTGAGCAAGTATATTACTGGGCACACCCTCCCCAGGCAGAGTGCCGCAGTTCCCTTAAGGGCAG 173712

Qy     1104 TGCCTGA 1110
            |||||||
Db   173713 TGCCTGA 173719
```

RESULT 12
AF308871

```
LOCUS       AF308871               1749 bp    mRNA    linear   VRT 02-JUN-2001
DEFINITION  Ambystoma mexicanum secreted factor Axwnt-8 (wnt-8) mRNA, complete
            cds.
ACCESSION   AF308871
VERSION     AF308871.1  GI:14280015
KEYWORDS    .
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 1749)
  AUTHORS   Bachvarova,R.F., Masi,T., Thomas,J., Hall,L. and Johnson,A.D.
  TITLE     Formation of posterior ventrolateral mesoderm in the urodele,
            Ambystoma mexicanum: expression of Axbra and Axwnt-8
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1749)
  AUTHORS   Bachvarova,R.F., Masi,T., Thomas,J., Hall,L. and Johnson,A.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-SEP-2000) Biological Science, Florida State
            University, Biology Unit I, Chieftan Way, Tallahassee, FL 32306,
            USA
FEATURES             Location/Qualifiers
     source          1. .1749
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
     gene            1. .1749
                     /gene="wnt-8"
     CDS             41. .1186
                     /gene="wnt-8"
                     /codon_start=1
                     /product="secreted factor Axwnt-8"
                     /protein_id="AAK58845.1"
                     /db_xref="GI:14280016"
                     /translation="MKNTKLFALTTLGVFCTIFTASAWSVNNFLMTGPKAYLYTSTSV
                     AVGAQSGIEECKFQFAWERWNCPESALQLSTHNGLRSATRETSFVHAISSAGWMYTLT
                     RNCSMGDFDNCGCDDSRNGRMGGRGWWNGGCSDNVFGGERISKFFVDALETGQDSRAL
                     MNIHNNEAGRFAVKSTMKRTCKCHGVSGSCSIQTCWLQLAEFRDIGNYLKIKHDQALK
                     LEMDKRMRAGNSADNRGAIAEAFSSLVATEILFLEDSPDYCLRNASLGLQGTEGREC
                     LQSGKNLSQWEKRSCRRLCTECGLKVEEKRTELVSSCNCKFHWCCTVKCEQCRQVVTK
                     HYCARKRDQSLNSNSNRRKHRTHSGNARARPLKEDLTGRRKMDVACVS"
BASE COUNT      465 a      407 c      456 g      421 t
ORIGIN

Query Match     48.5%;  Score 537.8;  DB 5;  Length 1749;
Best Local Similarity  72.0%;  Pred. No. 9.1e-149;
Matches 701;  Conservative  0;  Mismatches 272;  Indels  0;  Gaps  0;

Qy       95 TCTGGCTCACTTTTTCTCTTTTTGGTAGGTCAGTGAACAATTCCTGATAACAGGTCCCA 154
            ||||  | |||  | || |  ||  ||  ||||||||||| |||||  || |||||| |
Db       84 TCTGCACCATCTTCACCGGATCACAGCATGGTCTGTGAACAACTTCCTCATGACTGGTCCAA 143

Qy      155 AGGCCTATCTTGACCTACACGACTAGTGTGTGCCCTGGGTGCCCAGAGTGGCATCGAGGAGT 214
            ||| |||| || ||||| | |||  |||| || | |||| ||||||| |||||||||||| |
Db      144 AGGGCTACCTGACCTATTCCACCAGCGTGGCAGTGGGGGCTCAGAGCGGCATCGAGGAAT 203

Qy      215 GCAAGTTCCAGTTTGCCTGGGAACGGTGGAACTCCCCAGAAAATGCTTCTTCAGCTCTCCA 274
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      204 GCAAGTTCCAGTTTGCCTGGGAACGGTGGAACTCCCCAGAAAATGCTTCTTCAGCTCTCCA 263
```

```
Qy    275 CCCACAACAGGCTGAGAAGTGCTACCAGAGAGACWTTCCTTCATACATGCTATCAGCTCTG 334
          ||||||||||| ||||||||  |||||||||||| ||||||||||||||||||||||||||
Db    264 CCCACAACGGGACTGCGCAGCGCTACCAGGGGGAAAACGTTCCTTTGTGCACGGCCATCAGCTCGG 323

Qy    335 CTGGAGTCATTGTACATCATCACCAGAACTGTAGGCATGGGTGACTTCGAAAACTTGTGGCT 394
          ||||||||  |||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    324 CCGGAGTCAHTGTACACTCTGACCAGAACTGACCAGCATGGGCGGACTTCGACAACTCCGGCT 383

Qy    395 GTGATGGGTCAAACAATGGAAAACAGGAGGCCATGGCTGGATCTGGGGAGGCTGCAGCG 454
          |||||  ||| |||||   ||||||||||||||||  ||||||||||||||||||||||
Db    384 GTGACGACTCCAGAAATGCCCGCATGGGGTGGTCGCCGGATGGGTCTTCGGGAGGTTGCAGTG 443

Qy    455 ACAATGTGGAATTTGGGAAAGGGATCTCCAAAACTCTTTGTTGGACAGTTTGGAGGGGGA 514
          ||  ||||||||||||||||| ||||||||||| ||| ||||||||||||| |||||||
Db    444 ATAACGTCGACTTTGGAGAAAAGGAATTTCAAAATTTTTCGTAGATGCCCCTGGAGACTGGGCC 503

Qy    515 AGGATGCCAGGAGCCCTGATGAATCTTCAACACACAGGGGCCGGAGACTGGGCACGTGAGAG 574
          |||||| |||||| || ||||||| || |||| ||||| | ||||||  ||||||||||||
Db    504 AAGACTCAAGAGGCTTTTGATGAACACCCACAACAATGAAGCAGGGAGATTTGCTGTCAAAT 563

Qy    575 CCACCATGAAAAGGACATGCAAAATGTCATGCGCATCTCTGGGACTTGCGCAGCATACAGACAT 634
          |||||||||||  ||| ||||||||||||||||| || |||||||||| || |||||||
Db    564 CAACCATGAAGCGGACACTGCAAGTGCCACGGGGTGTCTCGGGAGCTGCCAGCCATTCAGGACCT 623

Qy    635 GCTGGCTGCAGCTGGGCTGCTGAATTCCCGGGAGACGATGGGAGACTACCTAAAGGCCAAGTATGACC 694
          ||||| |||||||   ||||||  ||||||||||||    ||||| ||||| ||||||  ||||||
Db    624 GCTGGCTGCAACTGCCGCAGAGTTCAGGGATATTAGGCCAATTAATCTGAAGATTTAAAACACGACC 683

Qy    695 AGGGCCTGAAAATTGAAAATGGAATAAGCGGGAGAGCTGAGAGTTGGGAAACAGCGCCGGAGGGGCC 754
          |||||||||||  ||||| ||||| ||| |||||   ||||||||  |||||||||||||| ||||
Db    684 AGGGCCTTGAAGCTCGAGATGGACACAAGCGCAGGATGGCGCCGCGCAACAGGGCCGACAACC 743

Qy    755 ACTGGGTGCCCGCTGAGGCCTTCTTCCTTCCTGAGCGCGAGAGGGGGGAACTGATCTTTTTTAGAGG 814
          ||||   || ||||||||||||   ||||||||||  |||||||| ||||||  |||| ||||||
Db    744 GCGGGGGCCATCGCGGAAGCCTTTAGCTCTTTGGTGGCGCAGCGACGCTTATCTTCCTTCCTGGAGG 803

Qy    815 AATCACCAGATTACTGTACCTGGCATCTGGGCACTCTATGGCACAGAGGGGTCGTG 874
          ||||| || ||||||||||||| |||  |||||| ||||||||||||||| ||||
Db    804 ACTGCGCCGGACTACTGCCTGAGAAACGCCAGGCTCCCAAGGCACCGAGGGGCCGGG 863

Qy    875 AGTGCCTACAGAGAACAGCCACAACACATCCAGGGTGTGGGGAGCCGAGCTGTGGGGGCCTGT 934
          |||| |||||||| ||||| |||||||||||||  ||| ||||| |  || |||||| || |
Db    864 AGTGCCTGCAGAGAGAGACCTTTCTCAGTGGGAAGAGAAGCTGCAGCGGCTGGCTGCTCT 923

Qy    935 GCACTGAGTGTGGGCGTGCAGGTGGGAAGAGGGAAAAACTGAGGTCATGAGGCTCTAACT 994
          |||||||||||   |||||||| ||||||||   ||||||  |||  ||||||||||
Db    924 GCACGGAGTGCGGCCCTGAAAGTGGAGGAGGAGGATGCGGTCGAAGCTCAGGCTGCAACT 983

Qy    995 GCAAATTCCAGTGGTGTCGGTCAAGTGTGACCAGTGTGTAGGCATGTGGCTGACGCAAGT 1054
          |||  ||| |||  ||||| |||||||| | |  ||| |||||||||||||| ||||||
Db    984 GCAAGTTTCACTGGTGCTGCACCGTGGTGGTGCGGCCGCAGGTGCGGTGACGAAGC 1043

Qy    1055 ATTACTGCGCACG 1067
           ||||| |||||||
Db    1044 ACTATTGCGCCG 1056
```

RESULT 13
AC021854/c

```
FEATURES             Location/Qualifiers
     source          1..144402
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="RP11-505H15"
     misc_feature    1..1445
                     /note="assembly_name:Contig10"
     misc_feature    1546..3851
                     /note="assembly_name:Contig11"
     misc_feature    3952..6428
                     /note="assembly_name:Contig12"
     misc_feature    6529..7846
                     /note="assembly_name:Contig13
                     clone_end:T7
                     vector_side:left"
     misc_feature    7947..10364
                     /note="assembly_name:Contig14"
     misc_feature    10465..13198
                     /note="assembly_name:Contig15"
     misc_feature    13299..15320
                     /note="assembly_name:Contig16"
     misc_feature    15421..18740
                     /note="assembly_name:Contig17"
     misc_feature    18841..22611
                     /note="assembly_name:Contig18"
     misc_feature    22712..26922
                     /note="assembly_name:Contig19"
     misc_feature    27023..32530
                     /note="assembly_name:Contig20"
     misc_feature    32631..39868
                     /note="assembly_name:Contig21"
     misc_feature    39969..47269
                     /note="assembly_name:Contig22"
     misc_feature    47370..55269
                     /note="assembly_name:Contig23
                     clone_end:SP6
                     vector_side:left"
     misc_feature    55370..62905
                     /note="assembly_name:Contig24"
     misc_feature    63006..70907
                     /note="assembly_name:Contig25"
     misc_feature    71008..81750
                     /note="assembly_name:Contig26"
     misc_feature    81851..96456
                     /note="assembly_name:Contig27"
     misc_feature    96557..112579
                     /note="assembly_name:Contig28"
     misc_feature    112680..129486
                     /note="assembly_name:Contig29"
     misc_feature    129587..144402
                     /note="assembly_name:Contig30"
BASE COUNT   40809 a   30400 c   30521 g   40644 t   2028 others
ORIGIN
```

```
   *   96557  112579: contig of 16023 bp in length
   *  112580  112679: gap of unknown length
   *  112680  129486: contig of 16807 bp in length
   *  129487  129586: gap of unknown length
   *  129587  144402: contig of 14816 bp in length.
```

```
Query Match       48.2%;   Score 535;   DB 2;   Length 144402;
Best Local Similarity  99.8%;   Pred. No. 9.1e-148;
Matches  546;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

Qy      564 GGCAGTGAGGAGGCCACCATGAAAAGGACACATCCAAATGTCATGGCATCTCTGGGAGCTGCAG 623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89759 GGCAGTGAGGAGGCCACCATGAAAAGGACACATCCAAATGTCATGGCATCTCTGGGAGCTGCAG 89700

Qy      624 CATACAGAGACATGCTGGCTGCTGCAGCTGCTGGCTGAATTCCGGGAGAGATGGGGAGACTACCTTAAAGGC 683
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89699 CATACAGAGACATGCTGGCTGCTGCAGCTGCTGGCTGAATTCCGGGAGAGATGGGGAGACTACCTTAAAGGC 89640
```

```
Qy      684 CAAGTATGACCAGGCCGCTGAAAATTGAAATGGATAAGCGGCAGCTGAGAGCTGAGAGCTGCAG 743
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89639 CAAGTATGACCAGGCCGCTGAAAATTGAAATGGATAAGCGGCAGCTGAGAGCTGAGAGCTGCAG 89580

Qy      744 CGCCGAGGCCCACTGGGTGCCCGGCTGAGCGCCTTCCTTCCTTAGCCGAGAGGCCCAGGAACTGAT 803
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89519 CGCCGAGGCCCACTGGGTGCCCGGCTGAGCGCCTTCCTTCCTTAGCCGAGAGGCCCAGGAACTGAT 89460

Qy      804 CTTTTTAGAGGAATCACCAGATTACTGTACCTGCCAAATTCCAGCCTGGGCCATCTATGGCAC 863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89459 CTTTTTAGAGGAATCACCAGATTACTGTACCTGCCAAATTCCAGCCTGGGCCATCTATGGCAC 89400

Qy      864 AGAGGGTCGTGAGTGCCTACAGAACAGCACCACAACATCCAGTGGGAGGACGGACGGTAGCTG 923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89399 AGAGGGTCGTGAGTGCCTACAGAACAGCACCACAACATCCAGTGGGAGGACGGACGGTAGCTG 89340

Qy      924 TGGGCGCCCTGTGCACTGAGTGTGGGCTGCAGTTGGTGGAAGAGACGGACGGACGGTCATAG 983
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89339 CAGCTGTAACTGCAAAATTCCAGTGGTGCTGTACGGTCAGGTGTGACCAGTGTAGGGCATGT 89280

Qy      984 CAGCTGTAACTGCAAAATTCCAGTGGTGCTGTACGGTCAGGTGTGACCAGTGTAGGGCATGT 1043
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    89279 GGGTGAGCAAGTATTACTGCGGCCACGGCTCCCAGGCAGCGAGTG-CCAGTCCCTGGGTAAGGGCAG 89221

Qy     1044 GGTGAGCAAGTATTACTGCGGCCACGGCTCCCAGGCAGCGAGTGCCAGTCCCTGGGTAAGGGCAG 1103
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db    89220 TGCCTGA 89214

Qy     1104 TGCCTGA 1110
            |||||||
Db    89220 TGCCTGA 89214
```

```
RESULT 14
XLXWNT8
LOCUS       XLXWNT8                1598 bp    mRNA     linear   VRT 11-MAY-1994
DEFINITION  X.laevis Xwnt-8 mRNA.
ACCESSION   X57234
VERSION     X57234.1   GI:486620
KEYWORDS    Xwnt-8 gene.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1
  AUTHORS   Christian,J.L., McMahon,J.A., McMahon,A.P. and Moon,R.T.
  TITLE     Xwnt-8, a Xenopus Wnt-1/int-1-related gene responsive to
            mesoderm-inducing growth factors, may play a role in ventral
            mesodermal patterning during embryogenesis
  JOURNAL   Development 111 (4), 1045-1055 (1991)
  MEDLINE   91347916
   PUBMED   1879349
REFERENCE   2
  AUTHORS   Moon,R.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JAN-1991) R.T. Moon, UNIVERSITY OF WASHINGTON, DEPT.
            OF PHARMACOLOGY, SJ-30, SEATTLE WA 98195, USA
REMARK      revised by [3] MAT
REFERENCE   3  (bases 1 to 1598)
  AUTHORS   Moon,R.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-1994) R.T. Moon, UNIVERSITY OF WASHINGTON, DEPT.
            OF PHARMACOLOGY, SJ-30, SEATTLE WA 98195, USA
COMMENT     On May 13, 1994 this sequence version replaced gi:65266.
FEATURES             Location/Qualifiers
     source          1..1598
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /dev_stage="neurula, stage 17"
     gene            1..1598
                     /gene="Xwnt-8"
```

```
CDS      55..1131
         /gene="Xwnt-8"
         /codon_start=1
         /protein_id="CAA40510.1"
         /db_xref="GI:486621"
         /db_xref="SWISS-PROT:P28026"
         /translation="MQNTTLFIIALTLLIFCPFFTASAVNNFLMTGPKAYLTYSASV
         AVGAQNGIEECKYQFAWERWNCPESTLQLATHNGLRSATRETSFVHAISSAGVMYLT
         RNCSMGPDRNCGCDDSRNGRIGGRGWVWGGCSDNAEFGERISKLFVDGLETGQDARAL
         MNLHNNEAGRLAVKETMRRTCKCHGISGSCSIQTCWLQLAERDIGNHLKIKHDQALK
         LEMDKRKMRSGNSAADNRGAIADAFSSVAGSELLFLEDSPDYCLRVEBKTEIISSCNK
         LQSGKNLSQWERSCKRLCTDCGLRVEEKKTEIISSCNKFHWCTVKCEQCKQVVIK
         HFCARRERDSNMLNTKRNRGHRR"
```

```
BASE COUNT      494 a     310 c     383 g     411 t
ORIGIN
```

```
Query Match     48.1%;  Score 533.6;  DB 5;  Length 1598;
Best Local Similarity  70.7%;  Pred. No. 1.6e-147;
Matches  710;  Conservative  0;  Mismatches  294;  Indels  0;  Gaps  0;
```

```
Qy    93 CCTCTGCCTCACTTTTCTCTTTTTGGTAGGTCAGTGAACAATTTCCTGATAACAGGTCC 152
         ||||||||||||||||||||||||||| ||| ||||||  ||||||  ||||||||||||
Db    96 CTTCTGCCCATTCTTCACTGCCTCAGCATGGTCAGTCAATTAACTTTCTGATGACAGGAC 155

Qy   153 CAAGCCTATCTGACCTACACGACTAGTTGTGTCCGCCTTGGGTGTGGCATCGAGGA 212
         ||||| |||||| |||||||||||||| || ||||||  ||||||||||||||||||
Db   156 CAAGGCATATCTGACTACTACCAGCGAGTTGCCGTGGGCGTGGGTGTGGCATGACGGAGGA 215

Qy   213 GTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTGCCCGGAAAAATGCTTCTTCAGCTCTC 272
         |||||||||||||||| || || |||| ||  ||  ||||||||||||  |||  |||||
Db   216 GTGTAAAATACAGTTTGCGTGGGAAAGATGGAATTGCCCTGAAAGTACCCCTGCCAGCTTGC 275

Qy   273 CACCCACACAGGCTGAGAAGTGCTACCAGGAGACTTCCTTCATACATGCTATCAGCTC 332
         || |||||||||| ||| |||||  || ||||||||||  |||  |||  ||||||||
Db   276 TACCCACAATGGACTTCGAAGTGCAACCAGAGAACCTCCTTTGTCATGCCATTCAGCTC 335

Qy   333 TGCTGGAGTCATGTGACATCACCAAGAACTGTGTAGCATGGGGTGGTGACTTCGAAAAACTGTGG 392
         |||| || |||||| |||  ||||||||||||||| ||| |||  ||||||||||||||
Db   336 AGCGGGAGTTATGTATACACTGACGAGAAACTGACGACTTTGATAACTGTGG 395

Qy   393 CTGTGATGGGTCAAACAATGGAAAAACAGAGGCCATGGCTGATGATCTGGGAGGGCTGCAG 452
         | |  ||| || ||  |||||||| ||||| |||||||  |||  |||||||||||||||
Db   396 ATGTGATGACTCCAGAAAATGCCCGCATCGGTGGCCGGGTTATGGGGGCGGGTTGCAG 455

Qy   453 CGACAAATGTGGGAAATTGGGGGAAAGGATCTCCAAACTCTTTGTGACAGTTTGGAGAAGGG 512
         || |||||||||| |||  |||| ||||||||||  |||||| |||||||||||||||
Db   456 TGATAAATGCACAGAATTTGGTCAGGCGGATGGCTTGGCTTGGGACGGG 515

Qy   513 GAAGGATGCCAGAGCCCTGATGAATCTTCACACACAGGCCGCGCAGAGCTGGCAGTGAG 572
         |||| |||| ||||||||||| |||| ||||||||||||  ||||||||||||||||
Db   516 ACAGATGCCACGAGCCCTAATGAACTGCATAACAATGAAGCAGGAAGACTTGCAGTGAA 575

Qy   573 AGCCACCATGAAAAACAGGACATGCAAATGTCATGGCATCTCTGGGACGTGCAGCATACAGAC 632
         ||||||  || ||||||||||||| |||  |||||||||  ||||||||||||||||||||
Db   576 AGAGCAATGCCAAGTGCCATGGCGAATATCTGGAATTGCGAGTGAAC 635

Qy   633 ATGCTGGTGGCTGCAGCTGGCTGAATTCCGGAGATGGGAGGACTACCTNAAGGCCAAGTATGA 692
         || ||||| || ||||||||||  || || |||||||||| ||  |||||||||||||
Db   636 TTGCTCGGGCTTCAGCTGCGATATTGGCAATCACTTAAAGAATCAAGCACGA 695

Qy   693 CCAGCGCGCTGAAAATTGAAATAAGCGCAGTTGAGAGCTGGGAACAGCGCCGAGGG 752
         ||||  | || |||| || ||| || || |||  |||  ||||||||||||||||
Db   696 CCAAGGCGCTGAAAGCTTGAGATGGACAGAGGAAAATGAGGTTAACACTGTCGACAA 755

Qy   753 CCACTCTGGGGTGCCCGGCCTTCCTTCCTTAGCCCGGAACTGATCTTTTTAGA 812
         || |||  |||||||||||  ||||||||  || ||||| ||  ||||||||
Db   756 CAGAGGAGGCCATCCGCTGGATCCTTCAGTTCTGTGCCGGGTCTGAACTTATT TTCTGA 815

Qy   813 GGAATCACCAGATTACTGTACCTGCAGAATTCCAGCCGTCATGGCACAGAGGTCG 872
         ||||||||| || ||||| |||||||| |||  ||| ||||||||||||||||
Db   816 AGACTCTCCGGATTATTGCTTAAAAACATCAGTTGCTGTTCTCCAGGGACAGAGGACG 875

Qy   873 TGAGTGCCTACAGAACAGCCACAACACATCCAGGTGGGACGGCCACTAGCTGTGGGCGGCCT 932
         |||||||||  |||||||||||  ||||||||| || |||  |||||||||||||||||
Db   876 AGAGTGCCTGCAAAGTGGCCAAGAACTTGTCCCAGTGGGACTTCCCAGTGGGAGAAGAAGCT 935
```

```
Db   933 GTGCACTGAGTGTGGGCTGAGCAGGTGGGAAAGAAAACTGAGTGTCATAAGCTTCCAGAGGCT 992
         ||||| ||||||||||||||||||||||| |||||||||||||| |||||||||||||||||
Qy   993 CTGCAAATTCCAGTGTGTCTACGGTCAAGTGTGCCAGGTGACCCAGTGTAGGCGATGTGGAGCA 1052

Db   936 TTGCACAGACTGGGCGGCCGCCTCCGGAGTGGAAGAGAAAAGACCGGAGATTATCAGTAGTAGCTGCA 995
         ||||  |||  |||  |||||||||||||||||||||||| |||||||||||||||||| |||
Qy   996 CTGCAAAATTCCACTCGGTTGCTCACACTCAAATGCCAGCCAATGCAAACAGGTTAGTGATAAA 1055

Db  1056 GCATTTCTGCCCCAGGAGGGGAACGGGGATTCCAACAATGCTGAATA 1099
         ||| |||| ||||||||||||| |||| |||||||||| |||||||
Qy  1053 GTATTACTCGGGCACCGCCTCCCCAGGCCAGTGCCCAGTGCCCTGGGTA 1096
```

```
RESULT 15
LOCUS       DRU10869    3022 bp    mRNA    linear    VRT 05-DEC-2001
DEFINITION  Danio rerio wnt8-like protein 1 and wnt8-like protein 2 (wnt8)
            mRNA, complete cds.
ACCESSION   U10869
VERSION     U10869.2  GI:14574562
KEYWORDS    .
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 10 to 1215)
  AUTHORS   Kelly,G.M., Greenstein,P., Erezyilmaz,D.F. and Moon,R.T.
  TITLE     Zebrafish wnt8 and wnt8b share a common activity but are involved
            in distinct developmental pathways
  JOURNAL   Development 121 (6), 1787-1799 (1995)
  MEDLINE   95324404
  PUBMED    7600994
REFERENCE   2  (bases 10 to 1215)
  AUTHORS   Kelly,G.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-1994) Pharmacology, University of Washington,
            Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 3022)
  AUTHORS   Lekven,A.C., Thorpe,C.J., Waxman,J.S. and Moon,R.T.
  TITLE     Zebrafish wnt8 encodes two wnt8 proteins on a bicistronic
            transcript and is required for mesoderm and neurectoderm patterning
  JOURNAL   Dev. Cell 1 (1), 103-114 (2001)
  MEDLINE   21563308
  PUBMED    11703928
REFERENCE   4  (bases 1 to 3022)
  AUTHORS   Lekven,A.C., Thorpe,C.J., Waxman,J.S. and Moon,R.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-2001) HHMI/Pharmacology, University of
            Washington, Box 357750, Seattle, WA 98195, USA
REMARK      Sequence update by submitter
COMMENT     On Jun 28, 2001 this sequence version replaced gi:968914.
FEATURES             Location/Qualifiers
     source          1..3022
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /chromosome="LGXIV"
                     /clone="wnt8"
                     /dev_stage="embryo"
     gene            1..3022
                     /gene="wnt8"
     CDS             23..1102
                     /gene="wnt8"
                     /codon_start=1
                     /product="Wnt8-like protein 1"
                     /protein_id="AAC59697.2"
                     /db_xref="GI:14574563"
                     /translation="MNPCQIFASLVMSICHILSSTAWSVNNFLMTGPKAYLAYTSSV
                     QAGAQSGIEECKIQFAWDRWNCPESALQLSTHKGLRSATRETAFVHAISAAGVMYTLT
```

```
                              GenCore version 5.1.6

                    Copyright (c) 1993 - 2004 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on:         January 30, 2004, 22:31:55 ; Search time 338 Seconds
                                             (without alignments)
                                             8865.018 Million cell updates/sec

Title:          US-09-898-456-6
Perfect score:  1110
Sequence:       1 atgctgtgctgcattcaagtg..........tgggtaagggcaggcctga 1110

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2552756 seqs, 134971901? residues

Total number of hits satisfying chosen parameters:    5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     N_Geneseq_19Jun03:*
               1:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
               2:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
               3:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
               4:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
               5:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
               6:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
               7:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
               8:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
               9:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
              10:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
              11:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
              12:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
              13:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
              14:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
              15:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
              16:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
              17:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
              18:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
              19:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
              20:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
              21:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
              22:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000A.DAT:*
              23:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
              24:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
              25:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
              24:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
              25:/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	% Score	Query Match	Length DB	ID	Description
1	989.6	89.2	1650	24	ABA05327	Human wingless-lik
2	988	89.0	1064	24	ABA04592	MOL4 coding sequen
3	986.4	88.9	1056	24	ABO86140	Novel human gene.
4	969.4	87.3	1245	22	AAD06571	Human Wnt3 (Zwnt3)
5	969.4	87.1	1245	22	ABS57866	Human cDNA encodin
6	708.4	63.8	1245	22	AAD06572	Human Wnt3 (Zwnt3)
7	708.4	63.8	1245	22	ABS57867	Human wingnut prot
8	434.6	39.2	1982	23	AAS76616	DNA encoding novel

```
 9  434.6  39.2  2119  25  AB281815  Ligand WNT-7A nucl
10  434.6  39.2  2119  25  AAD52543  WNT-8B DNA. Unide
11  434.6  39.2  2119  25  ABX75342  Human cDNA encoing
12  170   15.3  1195  20  AAX03794  Human Wnt-3 encodi
13  170   15.3  1195  25  AAD52572  WNT3 DNA. Unident
14  170   15.0  1194  25  ABX75313  Human cDNA encodin
15  166.8 15.0  1194  25  AB281810  Ligand WNT-2B nucl
16  162.6 14.7  1070  22  AAD20986  Human Wnt-7B-like
17  162.6 14.6  1082  24  ABK71909  Human cDNA encodin
18  162.6 14.6  1116  24  ABK71910  Human cDNA encodin
19  162.6 14.6  2932  25  AB234843  Coding sequence SE
20  153.4 13.8  2814  21  AAA88890  Mouse Wnt-3a gene.
21  153.4 13.8  2814  21  AA247790  Murine Wnt-3a enco
22  149.4 13.5  966   24  ABT08496  Human novel protei
23  149.4 13.5  1050  21  AAA64652  cDNA encoding a hu
24  145.8 13.1  1628  24  ABT08495  Human novel protei
25  144.6 13.0  1469  25  AB281814  Ligand WNT-6 nucle
26  144.6 13.0  1469  25  AAD52542  WNT-7A DNA. Unide
27  144.6 13.0  1469  25  ABX75317  Human cDNA encodin
28  144.2 13.0  1085  24  ABT06289  Human NOV8 coding
29  139.4 12.0  1402  24  ABK99935  DNA encoding human
30  133   12.0  1108  22  AAD16753  Human novel protei
31  132.4 11.9  1107  22  AAD16768  Human novel protei
32  129.2 11.6  1228  21  AAD20451  Wnt-4AF and Wnt-5c
33  129.2 11.6  1515  25  ABX62938  Human novel protei
34  129.2 11.6  1598  22  AAD16767  Human novel protei
35  128.8 11.6  1340  22  AAD90452  Wnt-4AF and Wnt-5c
36  128.2 11.6  1202  22  AAI58045  Human polynucleoti
37  128.2 11.5  2252  24  ABK92158  Prostate cancer-as
38  127.6 11.5  1598  22  AAI59831  Human polynucleoti
39  127.6 11.5  2049  20  AAI34081  Human PRO664 nucle
40  127.6 11.5  2049  21  AAC78505  Human PRO664 (UNQ4
41  127.6 11.5  2049  22  AAS45964  DNA encoding Human
42  127.6 11.5  2049  25  ACA57722  Human PRO664 cDNA.
43  127.6 11.5  2049  24  ABX98192  Human cDNA encodin
44  127.6 11.5  2049  25  ABX98694  Novel human secret
45  127.6 11.5  2049  25  ACA05739  Human secreted/tra
```

ALIGNMENTS

RESULT 1
ABA05327
ID   ABA05327 standard; DNA; 1650 BP.
XX
AC   ABA05327;
XX
DT   25-FEB-2002 (first entry)
XX
DE   Human wingless-like gene Wnt-8D SEQ ID NO 1.
XX
OS   Homo sapiens.
XX
KW   Human; wingless-like gene; Wnt-8D; antiasthmatic; nootropic; vaccine;
KW   neuroprotective; cytostatic; antidepressant; neuroleptic; vasotropic;
KW   cerebroprotective; vulnerary; asthma; Alzheimer's disease; cancer;
KW   cardiomyopathy; depression; schizophrenia; ischaemia; stroke;
KW   wound healing; kidney disease; lung disorder; apoptosis;
KW   stem cell therapy; immunological response; gene therapy; ds.
XX
FH   Key   Location/Qualifiers
FT   CDS   100..1155
FT   /tag= a
FT   /product= "Wnt 8D"
XX
PN   WO200183543-A1.
XX
PD   08-NOV-2001.
XX
PF   30-APR-2001; 2001WO-EP04887.
XX
PR   03-MAY-2000; 2000EP-0109422.

```
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Duecker K;
XX
DR   WPI; 2002-034504/04.
DR   P-PSDB; AAM47902.
XX
PT   New wingless/int 8D polypeptide, useful for treating asthma,
PT   Alzheimer's disease, cancer, ischaemia, stroke, depression,
PT   schizophrenia, aberrant apoptosis and for identifying modulators of
PT   polypeptide activity -
XX
PN   Claim 2; Page 35-37; 43pp; English.
XX
CC   The invention relates to a polypeptide, useful for treating asthma,
CC   wingless/int 8D (Wnt-8D) protein sequence of 351 amino acids (AAM47902)
CC   or is encoded by a defined polynucleotide sequence (II) of 1650
CC   nucleotides (ABA05327) or is a polypeptide having 95% identity to (I) or
CC   fragments or variants of above mentioned polypeptides. (I) has
CC   antiasthmatic, nootropic, neuroprotective, cytostatic, antidepressant,
CC   antiasthmatic, nootropic, neuroprotective, cytostatic, antidepressant,
CC   neuroleptic, vasotropic, cerebroprotective and vulnerary activity. (I) is
CC   useful for identifying compounds that stimulate or inhibit the function
CC   or level of the polypeptide. (I) and (II) are useful for treating asthma,
CC   Alzheimer's disease, cancer, cardiomyopathies, depression, schizophrenia,
CC   general psychotic disorders, ischaemia, stroke, wound healing, kidney
CC   diseases, lung disorders, aberrant apoptosis, tissue remodeling, stem
CC   cell therapies. (I) and (II) are also useful as vaccines for inducing an
CC   immunological response in a mammal and in gene therapy.
XX
SQ   Sequence 1650 BP; 423 A; 384 C; 460 G; 383 T; 0 other;

     Query Match             89.2%;  Score 989.6;  DB 24;  Length 1650;
     Best Local Similarity   99.6%;  Pred. No. 6.8e-304;
     Matches  992; Conservative  0; Mismatches  4;  Indels  0;  Gaps  0;

Qy     115 TTTGGTAAGGTCAGTGAAACAAATTTCCTGATAATAACAGTGTCCCAATGGCCTTATCTTACACG 174
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     160 TCTGCCTGGTCAGTGAACAAATTTCCTGATAACAGTGTCCCAATGGCCTATCTTACACG 219

Qy     175 ACTAGTGTGCGGCCTTGGGTGCCCAGAGTGGCATGAGGAGTGCAAGTTCCAGTTTGCTTGG 234
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 ACTAGTGTGCGGCCTTGGGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 279

Qy     235 GAACGCTGGAACTGCCCTGAAAATGTCTCTTCAGCTCTTCACCCACACAACAGGCTGAGAAGT 294
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280 GAACGCTGGAACTGCCCTGAAAAATGCTCTTCAGCTCTTCACCCACACAACAGGCTGAGAAGT 339

Qy     295 GCTACCAGAGAGACATTCCTTCATCATATGCTATACTCTCCTGCTGGAGTCATGTACATCATC 354
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     340 GCTACCAGAGAGACATTCCTTCATCATACATGCTATCAGCTCTCCTGGAGTCATGTACATCATC 399

Qy     355 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGAGGGTCAAACAAATGGA 414
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400 ACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGGTCAAACAAATGGA 459

Qy     415 AAAACAGGAGAGGCCATGGCTGGATCTGGGAGGAGGGCTGCAGCCAAATGGAATTTGGGGAA 474
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460 AAAACAGGAGAGGCCATGGCTGGATCTGGGAGGAGGGCTGCAGCCACAATGTGGAATTTGGGGAA 519

Qy     475 AGGGATCTCCAAACTCTTTTGTTGGACAGTTTGGAGAAGGGGAGAGGGGCCAGAGCCCTGATG 534
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     520 AGGATCTCCAAACTCTTTTGTTGGACAGTTTGGAGAAGGGGAGAGGATCCAGAGCCCTGATG 579

Qy     535 AATCTTCACACAACAACAGGGCGGCAGACTGGCAGTGAGAGCCACCATGAAAAGGACATGC 594
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     580 AATCTTCACACACAGGGCGGCAGACTGGCAGTGAGAGCCACCATGAAAAGGACATGC 639

Qy     595 AAATGTCATGGCATCTCTGGGGAGCTGCAGCATACAGACATGCTGGCTGCAGCTGGCTGAA 654
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     640 AAATGTCATGGCATCTCTGGGGAGCTGCAGCATACAGACATGCTGGCTGCAGCTGGCTGAA 699

Qy     655 TTCCGGGAGGATGGGAGGACTACCTAAAGGCCAAGTAGTGACCAGGCGGCTGAAAAATTGAAATG 714
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     700 TTCCGGGAGGATGGGAGGACTACCTAAAGGCCAAGTAGTGACCAGGCGGCTGAAAAATTGAAATG 759

Qy     715 GATAAGCGGCGAGCAGCTGGGAACAGGCCGAGGCCACTGGGTGCCCGAGGCC 774
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     760 GATAAGCGGCAGCTGAGAGCTGGGAACAGGCCGAGGCCACTGGGTGCCCGAGGCC 819

Qy     775 TTCCTTCCTAGCGCAGAGCGAGGCGGGAACTGATCTTTTTAGAGAGAATAACCAGATTACTGTACC 834
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     820 TTCCTTCCTAGCGCACAGAGGCGGGAACTGATCTCTTTTTAGAGAGAATCACCAGATTACTGTACC 879

Qy     835 TGCAATTCCAGCCTGGGCATTCTATGGCACAGAGAGGGTCGTGAGTGTGCCTACAGAACAGCCAC 894
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     880 TGCAATTCCAGCCTGGGCATTCTATGGCACAGAGAGGGTCGTGAGTGTGCCTACAGAACAGCCAC 939

Qy     895 AACACATCCAGGTGGGAGCGACGTAGCTTGTTGCTCGCCCTGTTGCACTGAGTGTGGGGCTGCAG 954
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     940 AACACATCCAGGTGGGAGCGACGTAGCTTGTTGGGGCCCTGTTGCACTGAGTGTGGGGCTGCAG 999

Qy     955 GTGGAAGAGAGAGGAAAACTGAGGTCATTAAGCACAGCGTAACTGCAAATTCCAGTGGTGGTTGCTGT 1014
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1000 GTGGAAGAGAGAGGAAAACTGAGGTCATTAAGCACAGCGTAACTGCAAATTCCAGTGGTGGTTGCTGT 1059

Qy    1015 ACGGTCAAGTGTGACCAGTGTTAGGCATGTGGTTGAGCAAGTATTTACTGCGCAGCTCCCCA 1074
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1060 ACGGTCAAGTGTGACCAGTGTTAGGCATGTGGTTGAGCAAGTATTTACTGCGCAGCTCCCCA 1119

Qy    1075 GGCAGTGCCCAGTCCCTGGGTTAAGGGCAGTGCCTGA 1110
           ||||||||||||||||||||||||||||||||||||
Db    1120 GGCAGTGCCCAGTCCCTGGGTTAAGGGCAGTGCCTGA 1155

XX
RESULT 2
ABA04592
ID   ABA04592 standard; cDNA; 1064 BP.
XX
AC   ABA04592;
XX
DT   21-FEB-2002  (first entry)
XX
DE   MOL4 coding sequence.
XX
KW   MOL; G-coupled protein-receptor; cardiomyopathy; atherosclerosis;
KW   cell signal processing; metabolic disorder; diabetes; cancer;
KW   neurodegenerative disorder; immune disorder; cardiac disorder;
KW   lung disease; autoimmune disease; developmental disorder; antidiabetic;
KW   Cytostatic; Neuroprotective; Antiatherosclerotic; Immunosuppressive;
KW   Gene therapy; Vaccine; antiinflammatory; MOL4;
KW   Wnt 8-like protein; 8s.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             4..1059
FT                   /*tag= a
FT                   /product= "MOL4"
XX
PN   WO200181578-A2.
XX
PD   01-NOV-2001.
XX
PF   26-APR-2001; 2001WO-US13578.
XX
PR   26-APR-2000; 2000US-200158P.
PR   28-APR-2000; 2000US-200613P.
PR   28-APR-2000; 2000US-200780P.
PR   01-MAY-2000; 2000US-201006P.
PR   01-MAY-2000; 2000US-201007P.
PR   01-MAY-2000; 2000US-201236P.
PR   01-MAY-2000; 2000US-201238P.
PR   02-MAY-2000; 2000US-201186P.
PR   03-MAY-2000; 2000US-201474P.
PR   03-MAY-2000; 2000US-201508P.
```

```
PR   25-JUL-2000; 2000US-220591P.
PR   15-SEP-2000; 2000US-232678P.
PR   22-JAN-2001; 2001US-263212P.
PR   30-JAN-2001; 2001US-265160P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Vernet CAM, Fernandes ER, Gerlach V, Shinkets RA, Malyankar UM;
PI   Boldog FL, Zerhusen BD, Spytek KA, Majunder K, Tchernev VT;
PI   Padigaru M, Patturajan M, Burgess CE, Gangolli EA, Smithson G;
PI   Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
PI   Alsobrook JP;
XX
DR   WPI; 2002-049278/06.
DR   P-PSDB; AAM47662.
XX
PT   Novel G-protein coupled receptor-related polypeptides and
PT   polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT   atherosclerosis, disorders related to cell signal processing and for
PT   identifying modulators -
XX
PS   Claim 8; Page 34; 227pp; English.
XX
CC   The present invention relates to novel G-coupled protein-receptor related
CC   proteins and coding sequences (MOLX, where X is a number from 1 to 10,
CC   ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
CC   sequences are useful for treating or preventing a MOLX-associated
CC   disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC   cell signal processing and metabolic pathway modulation, diabetes and
CC   cancer. Additionally, MOLX proteins and coding sequences are useful for
CC   preventing and treating a variety of disorders including metabolic
CC   disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC   obesity, infectious disease, anorexia, neurodegenerative disorders,
CC   Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC   haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC   and wasting disorders associated with chronic diseases and cancers,
CC   cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC   and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC   multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC   scleroderma, autoimmune diseases, developmental disorders and neural tube
CC   defects. The present sequence is the coding sequence for MOL4.
CC   MOL4 is a Wnt 8-like protein.
XX
SQ   Sequence 1064 BP; 269 A; 248 C; 323 G; 224 T; 0 other;

Query Match             89.0%;  Score 988;  DB 24;  Length 1064;
Best Local Similarity   99.5%;  Pred No 1.7e-303;
Matches   991;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    115 TTTGGTAGGTCAGTGGAACAAATTTCCTGATAACAGTCCCAAGGCCTATCTGACCTACACG 174
              ||||||||||||||| ||||||| |||||||||||||||||||||||||||||||||||
Db     64 TCTGCCTGTCAGTGAACAAATTCCTGATAACAGTCCCAAGGCCTATCTGACCTACACG 123

Qy    175 ACTAGTGTGGCCTTGGGTGCCCAGAGTGGCATGGAGGAGTGCAAGTTCCAGTTTGCTTGG 234
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 ACTAGTGTGGCCTTGGGTGCCCAGAGTGGCATGGAGGAGTGCAAGTTCCAGTTTGCTTGG 183

Qy    235 GAACGGCTGGAAACTCCCCTGAAAAAGTGCTTCTTCAGCTGTCTCCACCCACAACAGGAGT 294
              |||||||||||||||||| ||||| ||| | ||||||| ||||||||||||||  ||||
Db    184 GAACGGCTGGAAACTCCCTGAAAATGCTCTCTTCAGCTCTCCACCCACAACAGGCTGAGAAGT 243

Qy    295 GCTACCAGAGAGAGACTTCCTTCATACATGCTATACACTTCGGAGTCATGTACATCCATC 354
              ||||||||||| |||||||||||||||||||||||||| || |||||||||||||||||
Db    244 GCTACCAGAGAGACTTCCTTCATACATGCTATACACTTCAGCTCTGCATGTACATCATC 303

Qy    355 ACCAAGAACTGTAGCACTAGGGTGACTTCGAAAACTGTGGTGTGTGATGGGTCAAACAATGGA 414
              |||||||||||||||  | |||||||||||||||||||| |||||||||||||||||||||||
Db    304 ACCAAGAACTGTAGCCATGGGTGACTTCGAAAACTGTGGCTGTGTGATGGGTCAAACAATGGA 363

Qy    415 AAAACAGGAGGAGGGCCCATGGCTGGATCTGGGATGGGGGAGGGGGGGAAATTTGGGGAA 474
              |||| |||||||||||||||||||||||||||  |   || ||||  |||||||||||||
Db    364 AAAATAGGAGGAGGCCAATGGCTGGATCTGACTTCGACAATGTGGGAATTTCGGGGAA 423

Qy    475 AGGATCTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATG 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 AGGATCTCCAAACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGATGCCAGAGCCCTGATG 483

Qy    535 AATCTTCACAACACACAGGGCCCGGACGACTGAGGAGCCACCATGAAAAGGACATGC 594
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    484 AATCTTCACAACACACAGGGCCCGGACGACTGGCAGCCACCATGAAAAGGACATGC 543

Qy    595 AAAGTCATGGCATCTTCGGGAGCTCAGCATCAGACAGCATTGCTTGGCTGCAGCTGCGAA 654
              |||| |||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db    544 AAAATGTCATGGCATCTTCTCGGAGCTGCAGCATCAGACAGCATTGCTTGGCTGCAGCTGCGAA 603

Qy    655 TTCCGGGAGGATGGGAGGACTACCTAAAGGCCAAGTATGACCAAGGGGCTGAAAAATTGAAATG 714
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    604 TTCCGGGAGGATGGGAGGACTACCTAAAGGCCAAGTATGACCAAGGGGCTGAAAATTGAAATG 663

Qy    715 GATAAGCGGCAGCGTGAGAGCTGGGAAACAGCGGGCGGGGGCCCACTGGGTGCCCTGAGGCC 774
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    664 GATAAGCGGCAGCGTGAGAGCTGGGAACACAGCGGGCGGGGGCCCACTGGGTGCCCTGAGGCC 723

Qy    775 TTCCTTCCTPAGCCGCAGAGGGGGAACTGATCTTTTTTAGAGGAATCACCAGATTACTGTACC 834
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    724 TTCCTTCCTPAGCCGCAGAGGGGGAACTGATCTTTTTTAGAGGAATCACCAGATTACTGTACC 783

Qy    835 TGCAATTCCAGCCCTGGGCCATCTATGGCACAGAGGGGTCGTGAGTGCCTACAGAACAGCCAC 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 TGCAATTCCAGCCCTGGGCCATCTATGGCACAGAGGGGTCGTGAGTGCCTACAGAACAGCCAC 843

Qy    895 AACACATCCAGGTGGGACGACGTAGCTGTGTGGGCGCCCGTTGTCACTGAGTGTGGGCTGCAG 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    844 AACACATCCAGGTGGGACGACGTAGCTGTGTGGGCGCCCGTTGTCACTGAGTGTGGGCTGCAG 903

Qy    955 GTGGAAGAGAGGAAAACTGGAGGGTCATAAGCAGCAGCTGTAACTGCAAATTCCAGTGGTGCTGT 1014
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    904 GTGGAAGAGAGGAAAACTGGAGGGTCATAAGCAGCAGCTGTAACTGCAAATTCCAGTGGTGCTGT 963

Qy   1015 ACGGTCAAGTGTGACCAGCTGAGGCATGTGGTGAGCAAGTTACTACTGCGCACGCTCCCCA 1074
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    964 ACGGTCAAGTGTGACCAGCTGAGGCATGTGGTGAGCAAGTTACTACTGCGCACGCTCCCCA 1023

Qy   1075 GGCAGTGCCCAGTCCCTGGGTAAGGCAGTGCCTGA 1110
              |||||||||||||||||||||||||||||||||||
Db   1024 GGCAGTGCCCAGTCCCTGGGTAAGGCAGTGCCTGA 1059
```

RESULT 3

ABQ86140

```
ID   ABQ86140 standard; DNA; 1056 BP.
XX
AC   ABQ86140;
XX
DT   10-SEP-2002 (first entry)
XX
DE   Novel human gene. SEQ ID 11.
XX
KW   Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
KW   nootropic; neuroprotective; immunosuppressive; haemostatic;
KW   antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW   cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW   wound healing disorders; atherosclerosis; Parkinson's disease;
KW   Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW   inflammation; neoplastic disease; nervous system disorder;
KW   cardiovascular disorder; pancreatitis; respiratory disorder;
KW   hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW   developmental abnormality; gastrointestinal ulceration; neuropathy;
KW   haematological disease; metabolic disease; sperm dysfunction;
KW   thyroid disorder; hypothyroidism; brain damage; colitis;
KW   cone photo-transduction deficiency; neurological disease; stroke;
KW   angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW   trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW   growth abnormality; precocious puberty; gene; ss.
XX
OS   Homo sapiens.
```

```
PN   W02002050105-A1.
XX
PD   27-JUN-2002.
XX
PF   17-DEC-2000; 2001WO-US49232.
XX
PR   19-DEC-2000; 2000US-256710P.
PR   20-DEC-2000; 2000US-257048P.
PR   09-JAN-2001; 2001US-260482P.
PR   30-JAN-2001; 2001US-264922P.
PR   06-FEB-2001; 2001US-266797P.
PR   19-MAR-2001; 2001US-276988P.
PR   04-APR-2001; 2001US-281535P.
PR   08-MAY-2001; 2001US-289522P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;
PI   Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX
DR   WPI; 2002-508784/54.
DR   P-PSDB; ABP60975.
XX
PT   Secreted proteins and polynucleotides useful as vaccines for preventing
PT   or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT   Parkinson's disease, Alzheimer's disease, infection, autoimmune
PT   disorder -
XX
PS   Claim 2(a); Page 231; 335pp; English.
XX
CC   The invention relates to an isolated polypeptide with signal sequences
CC   which allow it to be secreted extracellularly or membrane associated.
CC   The activity of polypeptides of the invention may be described as,
CC   cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC   neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC   cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic,
CC   and metabolic. Polypeptides and polynucleotides of the invention are
CC   useful in the treatment, or as a vaccine in the prevention of, cancer,
CC   wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC   and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC   cardiovascular disorder, pancreatitis, respiratory disorder,
CC   hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC   developmental abnormality, gastrointestinal ulceration, neuropathy,
CC   haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC   disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC   transduction deficiency, neurological diseases, stroke, angiogenesis,
CC   ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC   trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC   growth abnormalities, and alleviation of precocious puberty. The
CC   sequences given in records ABQ86110-ABQ86184 represent novel human cDNA's
CC   of the invention.
XX
SQ   Sequence 1056 BP; 265 A; 247 C; 322 G; 222 T; 0 other;

     Query Match             88.9%;  Score 986.4;  DB 24;  Length 1056;
     Best Local Similarity   99.4%;
     Matches  990;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
                            Pred. No. 5.4e-303;

Qy         115 TTTGGTAGGTCAGTGAACAAATTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACG 174
                                 ||||||||||||||||||||||||||||||||||||||||
Db          61 TCTGCCTGGTCAGTGAACAAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACG 120

Qy         175 ACTAGTGTGGCCTTGGGTGCCCAGAGTGCAGAGTTCAGTTTGCTTGG 234
               ||||||||||||||||||||||||||||||||| ||||||||||||||
Db         121 ACTAGTGTGGCCTTGGGTGCCCAGAGTGCAGAGTTCCAGTTTGCTTGG 180

Qy         235 GAACGGCTGGAACTGCCCTGAAAAATCCTCTTCAGCTCTCCACCCACCCAACAGGCTGAGAAGT 294
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAACGGCTGGAACTGCCCTGAAAAATCCTCTTCAGCTCTCCACCCACCCAACAGGCTGAGAAGT 240
```

```
Qy         295 GCTACCAGAGAGACTTCCTTCATTCAGATTCATCACATGCTATCATCCTCGGAGTCATGTACATCATC 354
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCTACCAGAGAGACTTCCTTCATTCAGATTCATCACATGCTATCATCCTCGGAGTCATGTACATCATC 300

Qy         355 ACCAAGAACTGTAGCATGGGTGTGGTTCTGACTTCGGAATTCGAAAACTGTGGCTGTGATGA 414
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAGAACTGTAGCATGGGTGTGGTTCTGACTTCGGAATTCGAAAACTGTGGCTGTGATGA 360

Qy         415 AAAAACAGGAGGCCCATGGGTGTGGGGAGGCTGCGCAGCAACTGTGGCAATGTGGGGAA 474
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AAAAACAGGAGGCCCATGGGTGTGGGGAGGCTGCGCAGCAACTGTGGCAATGTTGGGGAA 420

Qy         475 AGGATCTCCAAAACTCTTTGTTGGACAGTTTGGAGAAGGGGAAGGGAACCCTGATG 534
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AGGATCTCCAAAACTCTTTGTTGGACAGTTTGGAGAAGGGGAAGGGAACCCTGATG 480

Qy         535 AATCTTCACAACACACAGGGCCCGCGGACGACTGGCAGTCACCACCATGAAAAGGACATGC 594
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 AATCTTCACAACAACAACAGGGCCGCGGACGACTGGCAGTCACCACCATGAAAAGGACATGC 540

Qy         595 AAAATGTCATGGCCATCTTCTGGGGAGTCAGAGATCAGACTGCAGCTGGCTGAA 654
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 AAAATGTCATGGCCATCTTCTGGGGAGTCAGAGATCAGACTGCAGCTGGCTGAA 600

Qy         655 TTCCGGGAGATGGGAGACATTACCTAAAAGGCCAAAGTCAGCGCCTGAAAAATTGAAATG 714
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TTCCGGGAGATGGGAGACATTACCTAAAAGGCCAAAGTCAGCGCCTGAAAAATTGAAATG 660

Qy         715 GATAAGCGGCCAGCTGAGAGCTGGGAAGCAGCGCCAGCGCCGGGTGCCGCTGAGGCC 774
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GATAAGCGGCCAGCTGAGAGCTGGGAAGCAGCGCCAGCGCCGGGTGCCGCTGAGGCC 720

Qy         775 TTCCTTCCTAGCGCAGAGGGGGACTGATCTTTTTGAGGAATCACCAGATTACTGTACC 834
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 TTCCTTCCTAGCGCAGAGGGGGACTGATCTTTTTGAGGAATCACCAGATTACTGTACC 780

Qy         835 TGCAATTCCAGCCTGGGCATCTATGGCACAGAGGGTCGTGAGTGCCTACAGAACAGCCAC 894
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TGCAATTCCAGCCTGGGCATCTATGGCACAGAGGGTCGTGAGTGCCTACAGAACAGCCAC 840

Qy         895 AACACATCCAGGTGGGAGCGACGTAGCTGTGGCGTGCTCACTGAGTGTGGGGCAG 954
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 AACACATCCAGGTGGGAGCGACGTAGCTGTGGCGTGCTCACTGAGTGTGGGGCAG 900

Qy         955 GTGGAAGAGGAGGAAAACTGAGGTCATAAGCACTGTAACTGCAAAATTCCAGTGGTGGCTGT 1014
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GTGGAAGAGGAGGAAAACTGAGGTCATAAGCACTGTAACTGCAAAATTCCAGTGGTGGCTGT 960

Qy        1015 ACGGTCAAGTGTGACCAGTGTAGGCCATGTGGTGACAAGTATTACTGCGACGCTCCCCA 1074
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 ACGGTCAAGTGTGACCAGTGTAGGCCATGTGGTGACAAGTATTACTGCGACGCTCCCA 1020

Qy        1075 GGCAGTGCCCAGTCCCTGGGTAAGGGCCAGTGCCTGA 1110
               |||||||||||||||||||||||||||||||||||||
Db        1021 GGCAGTGCCCAGTCCCTGGGTAAGGGCCAGTGCCTGA 1056
```

```
FH   Key              Location/Qualifiers
FT   CDS              1..1245
FT                    /tag= a
FT                    /product= "Zwnt3 protein"
FT                    /transl_except= (pos:511..513, aa:Ala)
FT                    /note= "CDS does not include stop codon"
FT                    /partial
XX
PN   WO200138353-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US31820.
XX
PR   22-NOV-1999;  99US-0444788.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Holloway JL;
XX
DR   WPI; 2001-367660/38.
DR   P-PSDB; AAB02906.
XX
PT   Zwnt3 polypeptides useful for producing antibodies, for
PT   biopharmaceuticals, and as educational tools in laboratory practical
PT   kits -
XX
PS   Claim 6; Page 75-77; 82pp; English.
XX
CC   The present sequence is a cDNA encoding human Wnt3 (Zwnt3) protein which
CC   is a cellular signalling molecule. Wnt proteins are a family of secreted
CC   glycoproteins, which, in many organisms, have a role in morphological
CC   development of tissues in both embryonic and adult contexts. Wnt3 DNA
CC   and protein are useful as education tools in laboratory practical kits
CC   for genetics and molecular biology, protein chemistry and antibody
CC   production, and analysis. Wnt3 protein is useful as an aid to teach
CC   preparation of antibodies, identify proteins by Western blotting,
CC   protein purification, determining the weight of expressed Zwnt3
CC   polypeptides as a ratio of total protein expressed, identifying peptide
CC   cleavage sites, coupling amino acids and carboxyl terminal tags, amino
CC   acid sequence analysis and monitoring biological activities of both
CC   native and tagged protein in vitro and in vivo. Ab is useful for
CC   purifying Zwnt3, and cloning and sequencing the polynucleotides that
CC   encodes an antibody, hence in the design of humanised antibodies.
CC   Wnt3 DNA is also useful in gene therapy.
XX
SQ   Sequence 1245 BP; 318 A; 306 C; 347 G; 274 T; 0 other;

Query Match             87.3%;  Score 969.4;  DB 22;  Length 1245;
Best Local Similarity   99.4%;
Matches  973;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy          115 TTTGGTAGGTCAGTGAACAATTTCCTGATAACAGTCCCAAGGCCTATCTGACCTACACG 174
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 TCTGCCTGTGTCAGTGAACAATTTCCTGATAACAGTCCCAAGGCCTATCTGACCTACACG 120

Qy          175 ACTAGTGTGGCCTTGGGTGCCCAGAGTGGCATCGAGGAGTGCCAAGTTCCAGTTTGCCTGG 234
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 ACTAGTGTGGCCTTGGGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCCTGG 180

Qy          235 GAAGGCTGAAACTGCCCTGAAAAATGCTCTTCTTCAGCTCTCCACCCACAAACAGGCTGAGAAGT 294
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GAACGCTGAAACTGCCCTGAAAAATCCTCTTCAGCTCTCCACCCACAAACAGGCTGAGAAGT 240

Qy          295 GCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTTCCTGGAGTCATGTGTAACATCATC 354
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 GCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTTCCTGGAGTCATGTGTAACATCATC 300

Qy          355 ACCAAGAACTGTAGCATGGGTTGACTTCGAAAACTGTGGTGTCAAAACAAATGGA 414
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 ACCAAGAACTGTAGCATGGGTTGACTTCGAAAACTGTGGTGTCAAAACAAATGGA 360

Qy          415 AAAACAGGAGGAGCCATGGCTGGGATCTGGGGAGGCTGCAGCAGACAATGTGGAATTGGGGGAA 474
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AAAACAGGAGGAGCCCATGGGTCGGATCTGGTCGATCTGGGGAGGAGGCTGCGACAATGTGGAATTTGGGGAA 420

Db          421 AGGATCTCCAAAACTCTTTGTGGACAGTTGGGAGGAGAGGGGGAAGGGGCTGGTCGACAGTTGGAATGGTGGGG 480

Qy          475 AGGATCTCCAAAACTCTTTGTGGACAGTTGGGAGGAGAGGGGGAAGGGGCTGGTCGACAGTTGGAATG 534
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 AATCTTCACACACAACAGGGGCCCGGCAGACTGGTGTGGTGGAGGCCACCATGAAAAGGACATGC 540

Qy          535 AATCTTCACACACAACAGGGGCCCGGCAGACTGGTGTGGTGGAGGCCACCATGAAAAGGACATGC 594

Db          541 AAAATGTCATGGCATCTCTCGGGAGCTGCAGCATACAGACACATGCTGGCTGCGCTGGCTGGCTGAA 600

Qy          595 AAAATGTCATGGCATCTCTCGGGAGCTGCAGCATACAGACACATGCTGGCTGCGCTGGCTGGCTGAA 654

Db          601 TTCCCGGGAGATGGGGAGACTACCTAAAAGGCCAAGTATGACCAGGGGGCTGAAAATTGAAATG 660

Qy          655 TTCCCGGGAGATGGGGAGACTACCTAAAAGGCCAAGTATGACCAGGGGGCTGAAAATTGAAATG 714

Db          661 GATAACCGGGCAGCTGAGAGTGGGAACACAGCAGCGGCCGCCGGCTAAAAGGCCCACCTGGGTGGC 720

Qy          715 GATAACCGGGCAGCTGAGAGTGGGAACACAGCAGCGGCCGCCGGCTAAAAGGCCCACCTGGGTGGC 774

Db          721 TTCCTTCCTTCAGCGCAGAGGGGGGAACTGGGCCGAGGGGCCGAGGCC 780

Qy          775 TTCCTTCCTAGCGCAGAGGGGGGAACTGGGCCGAGGGGCCCACCAGATTACTGTACC 834

Db          781 TGCAATTCCAGCCTGGGCATCTATGCACAGAGGGGTCGTGAGTGCCTACAGACAACAGCCAC 840

Qy          835 TGCAATTCCAGCCTGGGCATCTATGCACAGAGGGGTCGTGAGTGCCTACAGACAACAGCCAC 894

Db          841 AACACATCCAGGTGGGAGCCACGTTAGCTGTGTGGGCGGCTGTGTGCACTGAGTGTGTGGCGCAG 900

Qy          895 AACACATCCAGGTGGGAGCCACGTTAGCTGTGTGGGCGGCTGTGTGCACTGAGTGTGTGGCGCAG 954

Db          901 GTGGAAGAGGAGAAAACTGAGGTCATAAGCAGCGTTAACTCCAAATTCCAGTGGTGGTCGTGT 960

Qy          955 GTGGAAGAGGAGAAAACTGAGGTCATAAGCAGCGTAACTCCAAATTCCAGTGGTGGTCGT 1014

Db          961 ACGGTCGAAGTGTGACCAGTGTAGGCATGGTGGTGATTACTGCGCACGGCTCCCA 1020

Qy         1015 ACGGTCAAGTGTGACCAGTGTAGGCATGGTGGTGATTACTGCGCACGGCTCCCA 1074

Db         1021 GGCCAGTGCCCAGTCCCTGG 1039

Qy         1075 GGCCAGTGCCCAGTCCCTGG 1093
```

RESULT 5
ABS57866
ABS57866;
ABS57866 standard; cDNA; 1245 BP.
07-FEB-2003 (first entry)
ABS57866;
Human cDNA encoding wingnut protein Zwnt3.
Human; wingnut; ss; gene; Zwnt3; signalling molecule;
secreted glycoprotein; extracellular matrix; tumour; brain development.
Homo sapiens.

```
Key              Location/Qualifiers
CDS              1..1245
                 /tag= a
                 /product= "Zwnt3"
                 /partial
                 /note= "No stop codon shown"
misc_feature     694..741
                 /tag= b
                 /note= "This region is claimed in claim 6"
misc_feature     961..1245
```

```
FT
FT         /tag= c
XX         /note= "This region is claimed in claim 6"
PN    US20021231O3-A1.
XX
PD    05-SEP-2002.
XX
PF    03-DEC-2001; 2001US-0005947.
XX
PR    22-NOV-1999;        99US-168827P.
PR    17-NOV-2000; 2000US-0715993.
XX
PA    (HOLL/) HOLLOWAY J L.
XX
PI    Holloway JL;
XX
DR    WPI; 2003-066796/06.
DR    P-PSDB; ABG72362.
XX
PS    Claim 8; Page 29-31; 37pp; English.
XX
CC    Novel human Zwnt3 polypeptide useful as aid for identifying proteins by
CC    Western blotting, to teach analytical skills such as mass spectrometry
CC    and circular dichroism, and for identifying peptide cleavage sites -
CC
CC    The invention relates to an isolated human Zwnt3 polypeptide (a wingnut
CC    protein which is a signalling molecule/secreted glycoprotein, found
CC    in the extracellular matrix) that is at least 80% identical to
CC    the protein appearing as ABG72362 sequence (S1) of 415 amino acids,
CC    where the polypeptide specifically binds with an anti-Zwnt3
CC    antibody, or its fragments. Also included are the Zwnt3 encoding
CC    nucleic acid (or portion), expression vectors, a recombinant host cell
CC    comprising the vector, the antibody, using Zwnt3 probes to detect
CC    Zwnt3 mRNA in a biological sample, an anti-idiotype antibody that
CC    binds the anti-Zwnt3 antibody and Zwnt3 fusion proteins.
CC    Wnt overexpression can lead to tumour formation and they are
CC    involved in brain development. Zwnt 3 is useful as an aid for identifying
CC    proteins by Western blotting, protein purification, determining the
CC    weight of the expressed Zwnt3 polypeptides as a ratio to total protein
CC    expressed, and for identifying peptide cleavage sites and to teach
CC    analytical skills such as mass spectrometry, circular dichroism, to
CC    determine conformation, especially of the four alpha helices, x-ray
CC    crystallography to determine the three-dimensional structure in atomic
CC    detail, nuclear magnetic resonance spectroscopy to reveal the structure
CC    of proteins in solution. Zwnt3 is further useful in treating
CC    a subject who lacks an adequate amount of the protein, and also in
CC    veterinary and human therapeutics. The nucleic acids are useful as
CC    polymerase chain reaction (PCR) primers and probes, and to detect the
CC    expression of a Zwnt3 gene in biological sample, and also to determine
CC    whether a subject's chromosomes contain a mutation in Zwnt3 gene.
CC    The present sequence is the cDNA encoding human Zwnt3.
XX
SQ    Sequence 1245 BP; 318 A; 306 C; 347 G; 274 T; 0 other;

Query Match             87.3%;  Score 969.4;  DB 25;  Length 1245;
Best Local Similarity   99.4%;
Matches  973;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;
```

```
Qy          115 TTTGGTAGGTCAGTGAACAACAAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACG 174
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 TCTCCCTGCGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACG 120

Qy          175 ACTAGTGTGGCCTTGGGGTCGGCATCGAGGAGTGGCAAGTTCCAGTTTGCCTTGG 234
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 ACTAGTGTGGCCTTGGGGTCGGCATCGAGGAGTGGCAAGTTCCAGTTTGCCTTGG 180

Qy          235 GAACGCTGGAACTGCCCTGAAAAAGTCTCTTCCTCAGGAGTGGCAAGTTCCAGTTTCCTTGG 294
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GAACGCTGGAACTGCCCTGAAAAATCCTCTTCAGCTCCACCCACAACAGGCTGAGAAGT 240

Qy          295 GCTACCAGAGAGACTTCCTTCATACATGCTATCACTTCAGCTCCACCCACAACAGGCTGAGAAGTTACATTCATC 354
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 GCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCCTGGAGTCAGTGAGTTACATTCATC 300
```

```
RESULT 6
AAD06572
ID    AAD06572 standard; cDNA; 1245 BP.
XX
AC    AAD06572;
XX
DT    10-AUG-2001  (first entry)
XX
DE    Human Wnt3 (zWnt3) cDNA degenerate sequence.
XX
KW    Human; Zwnt3; gene therapy; cellular signalling; antibody production;
KW    tissue development; biopharmaceutical; glycoprotein; education tool; ss.
OS    Homo sapiens.
XX
PN    WO200138353-A2.
XX
PD    31-MAY-2001.
XX
```

```
Qy          355 ACCAAGAAACTGTAGCACATGGGGTGACTTCGAAAAACTGTGGCTGTGATGGGTCAAATGGA 414
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 ACCAAGAAACTGTAGCACATGGGGTGACTTCGAAAAACTGTGGCTGTGATGGGTCAAATGGA 360

Qy          415 AAAACAGGAGCGAGGCCATGGGGCTGGATCTGGGAGGCTGGGCTGCGACAAATGTGGAATTTGGGGAA 474
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AAAACAGGAGCGAGGCCATGGGGCTGGATCTGGGAGGCTGGGCTGCGACAAATGTGGAATTTGGGGAA 420

Qy          475 AGGATCTCCAAAACTCTTTGTGGGACAGTTTGGAGAAGGGGAAGGGAATGCCAGAGCCCTGATG 534
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 AGGATCTCCAAAACTCTTTGTGGGACAGTTTGGAGAAGGGGAAGGGAATGCCAGAGCCCTGATG 480

Qy          535 AATCTTCACAACAACAGGGCCGGACAGCAGCTGGCAGTGAGACCCACCATGAAAAGGACATGC 594
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 AATCTTCACAACAACAGGGCCGGACAGCAGCTGGCAGTGAGACCCACCATGAAAAGGACATGC 540

Qy          595 AAAATGTCATGGCATCTTCTGGGAGCTTGGCAGCATACAGATACAGCTGCTGCTGCTGAA 654
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 AAATGTCATGGCATCTTCTGGGAGCTTGGCAGCATACAGATACAGCTGCTGCTGCTGAA 600

Qy          655 TTCCGGGAGATGGGAGGAGACTACCTAAAAGGCCAAGTAAGGCCAAGTAATGACAGAGCCTG 714
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 TTCCGGGAGATGGGAGGAGACTACCTAAAAGGCCAAGTATGACAGAGCCTGAAAATTGAAAATG 660

Qy          715 GATAAGCGGCAGCTGAGAGCTGGGAAACAGCCCCGAGGGCCCACTCGGGTGCCCGCTGAGGCC 774
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 GATAAGCGGCAGCTGAGAGCTGGGAAACAGCCCCGAGGGCCCACTCGGGTGCCCGCTGAGGCC 720

Qy          775 TTCCTTCCTAGGCGCAGAGGCGGGAACTGACTCTTTTTAGAGGAATCACCAGATTACTGTACC 834
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 TTCCTTCCTAGGCGCAGAGGCGGGAACTGACTCTTTTTAGAGGAATCACCAGATTACTGTACC 780

Qy          835 TGCAATTCCAGCCTGGGCATCTATGGCACAGAGGGTCGTGAGTGCGTCGTACGAGAACAGCCAC 894
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 TGCAATTCCAGCCTGGGCATCTATGGCACAGAGGGTCGTGAGTGCGTCGTACGAGAACAGCCAC 840

Qy          895 AACACATCCAGGTGGGAGCGACGTAGCTGTTGGGCGCGCCGCTGTCACTGAGTGTGTGGGCTGCAG 954
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 AACACATCCAGGTGGGAGCGACGTAGCTGTTGGGCGCCGCTGTGCACTGAGTGTGTGGGCTGCAG 900

Qy          955 GTGGAGAGAGGAAAACTGAGGTCATAAGGACTGTAACTGCAAAATTCCAGTGGTGGTGCTGT 1014
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GTGGAGAGAGGAAAACTGAGGTCATAAGGACTGTAACTGCAAAATTCCAGTGGTGGTGCTGT 960

Qy         1015 ACGGTCAAGTGTGACCAGTGTTGAGGCATGTGGTGACGAAGTAATTACTGCGACGCGTCCCCA 1074
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 ACGGTCAAGTGTGACCAGTGTTGAGGCATGTGGTGACGAAGTAATTACTGCGACGCGTCCCCA 1020

Qy         1075 GGCAGTGCCCAGTCCCTGG 1093
                |||||||||||||||||||
Db         1021 GGCAGTGCCCAGTCCCTGG 1039
```

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 23:40:10 ; Search time 94 Seconds
(without alignments)
5212.077 Million cell updates/sec

Title: US-09-898-456-6
Perfect score: 1110
Sequence: 1 atgctcgtgcgcattcaagtg...........tgggtaaggcagtgcctga 1110

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	170	15.3	1195	3	US-09-082-270-1	Sequence 1, Appli
2	149.4	13.5	1050	3	US-09-459-774-1	Sequence 1, Appli
3	149.4	13.5	1050	4	US-09-903-817-1	Sequence 1, Appli
4	126.6	11.4	2057	3	US-09-082-089-4	Sequence 4, Appli
5	126.6	11.4	2190	3	US-09-082-089-1	Sequence 1, Appli
6	123.2	11.1	1056	3	US-09-067-782A-1	Sequence 1, Appli
7	119	10.7	478	3	US-09-082-270-3	Sequence 3, Appli
8	92.6	8.3	2122	1	US-08-485-449-1	Sequence 1, Appli
9	75.8	6.8	850	4	US-09-449-285A-8	Sequence 8, Appli
10	66.4	6.0	1272	1	US-08-647-928-7	Sequence 7, Appli
11	65.6	5.9	4522	5	PCT-US93-06251-22	Sequence 22, Appl
12	63.8	5.7	7218	1	US-08-232-463-14	Sequence 14, Appl
13	58	5.2	1748	1	US-08-485-449-3	Sequence 3, Appl
14	48	4.3	439	1	US-09-067-782A-3	Sequence 3, Appli
15	37.2	3.4	7218	1	US-09-232-463-14	Sequence 14, Appl
16	36.6	3.3	468	1	US-09-067-782A-6	Sequence 6, Appli
17	35.4	3.2	289	3	US-09-007-005-17	Sequence 17, Appl
18	35.4	3.2	289	1	US-09-244-796-17	Sequence 17, Appli
19	34.8	3.1	732	4	US-09-252-991A-961	Sequence 961, App
20	34.8	3.1	1835	4	US-09-620-312D-200	Sequence 200, App
21	34.8	3.1	2505	4	US-09-252-991A-1045	Sequence 1045, Ap
22	34.4	3.1	1700	5	PCT-US92-02091-1	Sequence 1, Appli
23	34	3.1	592	6	US-09-5166058-1	Patent No. 5166058
24	34	3.0	1055	2	US-08-468-012A-1	Sequence 1, Appli
25	33.2	3.0	1055	4	US-09-054-989-1	Sequence 1, Appli
26	33.2	3.0	1055	4	US-09-662-746A-1	Sequence 1, Appli
27	33	3.0	1269	4	US-09-252-991A-5428	Sequence 5428, Ap
28	33	3.0	1990	1	US-08-454-720A-35	Sequence 35, Appl
29	33	3.0	13953	4	US-09-738-884-3	Sequence 3, Appli
30	32.8	3.0	7676	1	US-08-451-777A-7	Sequence 7, Appli
31	32.8	3.0	7676	2	US-08-998-208-7	Sequence 7, Appli
32	32.8	3.0	7676	2	US-09-252-991A-4008	Sequence 4008, Appli
33	32.8	3.0	7676	5	PCT-US95-06743-7	Sequence 7, Appli
34	32.8	3.0	478	5	US-09-643-597-119	Sequence 119, App
35	32.6	2.9	8948	4	US-09-480-884A-119	Sequence 119, App
36	32.6	2.9	8948	4	US-09-542-615A-119	Sequence 119, App
37	32.6	2.9	8948	4	US-09-606-421B-119	Sequence 119, Appl
38	32.6	2.9	12597	4	US-09-705-299-12	Sequence 12, Appl
39	32.6	2.9	1230025	4	US-09-198-452A-1	Sequence 1, Appl
40	32.4	2.9	592	3	US-07-721-847A-1	Sequence 1, Appli
41	32.4	2.9	1731	4	US-08-925-779-1	Sequence 1, Appli
42	32.4	2.9	592	4	US-09-252-991A-4008	Sequence 4008, Ap
43	32.4	2.9	2472	4	US-09-252-991A-3902	Sequence 3902, Ap
44	32.4	2.9	2562	4	US-09-252-991A-4045	Sequence 4045, Ap
45	31.8	2.9	1088	3	US-09-077-675A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-082-270-1
Sequence 1, Application US/09082270
; Patent No. 6043053
; GENERAL INFORMATION:
; APPLICANT: TESTA, TANIA
; APPLICANT: BARNES, MICHAEL
; TITLE OF INVENTION: No. 6043053e1 Compounds
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,270
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9710716.3
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: GB 9804921.6
; FILING DATE: 06-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30164
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-082-270-1

Query Match   15.3%;   Score 170;   DB 3;   Length 1195;
Best Local Similarity   54.2%;   Pred. No. 8.4e-44;
Matches   413;   Conservative   0;   Mismatches   340;   Indels   9;   Gaps   3;

Qy   171 CACGACTAGTGTTGTGGCCTTGGGTGCCCAGAGTGGGCATCGAGGAGTGCCAAGTTCCAGTTTGC 230
Db   314 CATGCCACGGGTGGGCGCTGGAAGCGTGAAAGCTGGGCATCCAGGAGTGCCAGACCAGTTCCG 373

Qy   231 TTGGGAAACGGCTGGAACTGCCCTGAAAAATGCTTCTTCAGCTCTTCCACCCACAA---CAGGCT 287
Db   374 GGGCGCCGGCTGGAACTGCACCACCATAGAATGACAGCCTGGCCATCTTTTGGGCCGTCCT 433

Qy   288 GAGAAGTGTGCTACCAGAGAGACTTCCTTCATACATTCTATCAGCTCTTGCTGCTGTCATGTA 347
Db   434 CGACAAAGCCACCCCGGGAGTCGGGCCTTCGTTCACCCAATGGCGCCATCTGGATGGGGCCTT 493

Qy   348 CATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTTGTGGGTTCAAA 407
Db   494 CGCCCGTCACCCGGCTCCTGCCCGCGGAGGCACCTCACCATTTGCGCGGTGACTCGGCATCA 553

Qy   408 CAATGGGAAAAACAGAGGAGGCCATGGGTGGATCTCGGGGGAGGGCTGCAGGCCGACAAATGTGGGAATTC 467
Db   554 TAAGGG---GCCGGCTGGCCGAAGGCCTGGGAAGTGGGGGGGGTCGGCGAGAGCGCTGACTT 610

Qy   468 TGGGGAAAGGGAGGATCTCCAAAACTTCTTTGTGGACAGTTTGGGGGAGGGGGAAGGAGGATCTCCAAA 527
Db   611 CGGGCGTGTTAGTGTGCCAGGGAGTTCCCGGATNGGCCCGAGACCAGGCCGGAACAGCGCCGGCTC 670

Qy   528 CCTGGATGAATCTTCACCAACAACAGCAGCCGGCCAGTGAGGCCACCATCGAAAAG 587
Db   671 GGCCATGAACAAGCACAACAAACGAGGGCCGCACGACTATCCTGGACCACATCCACCT 730

Qy   588 GACATGCAAATGTCATGGGCCATCTCTGGGAGCTGCAGCATACAGACTACGAGACTGGCTGGCTGGCAGCT 647
Db   731 CAAATGCAAGTGCCACGGGCTGTCCCGGCCTGCCAGCTGTTGCTGGTGTGGGGCCA 790

Qy   648 GGCTGAATTCCGGGAGAGATGGGAGACTACTTAAAGCCCAACTATATGACCGAGCGCGCTGAAAAT 707
Db   791 GCCTGACTTCCCGTGCCATCCGGTGACTTCCTCAAGGACAATGGCGGGCGCCCTCGGAGAT 850

Qy   708 TGAAAATGGATNAAGCGGCAGCTGGGAACAGCGCCGGAGGGGCCACTGGGGTGCCCGC 767
Db   851 GGTAGTAGAGAA---GCACCGTGACTCCCGAGGCTGGGGTGGAGAGGGCGGCCACTGGGGTGCCCGC 907

Qy   768 TGAGGCCTTCCTTCCTTCCTAGCCGCGGAGGCGGGAACTGATTCTTTTAGGGGAATCACCAGATTA 827
Db   908 CTCGGCTCTTCAAGCCACACCCACCTGGTCTACTACGGAGGAACTCCCCCAACTT 967

Qy   828 CTGTACCTGCAAATTCCAGCGTCGGGCATCTATGGGCACAGAGAGGGGTGTCGTGAGTGCCTACAGAA 887
Db   968 TTGTGAGCCCAACCCAGAGACGGGGTTCCTTTGGCACAAGGGACCGGACTTGCAATGTCAC 1027

Qy   888 CAGCCACAACACATCCAAGGTGGGAGGGGGGGGGACCTAGCTGTGGGGCG 929
Db   1028 CTCCACGGCCATCGATGGCTGCGATCTGCTCTGCTGTGGGGCCG 1069

US-09-459-774-1

Query Match   13.5%;   Score 149.4; DB 3; Length 1050;
Best Local Similarity 52.0%; Pred. No. 2.7e-37;
Matches 386; Conservative 0; Mismatches 351; Indels 6; Gaps 2;

Qy   190 GGTGCCCAGAGTGGCAATCGAGGAGTGCAAGTTCCAGTTTGCTTGGGAACGGCTGGAACTGC 249
Db   193 GGCTCACAAATGGGCCTGGACGGAGTGTCAGTTTCAGTTTCCGGACGTTGGGAACTGC 252

Qy   250 CCTGAAAATGCTTCTTCAGCTCTTCCACCCACAACAGCAGGTGAGAAGTGCTACCAGAGACT 309
Db   253 TCTGCACTGGGAGACGGCACCGTCTTCGGAGAAGGAGCTCAAAGTGGGGAGGGGGAGGCT 312

Qy   310 TCCTTCATACATGCTATCAGCTCTTGCTGCTGTCATGTACATCATCACCAAGAACTGTAGC 369
Db   313 GCGTTCACCTACGCCATCATTGCCCCGCGCCGGCCGCCATCACAGCTGCCTGTACC 372

Qy   370 ATGGGTGACTTCGAAAAACTGTGGGTTCAAACAATGG---AAAAACAGGAGGC 426
Db   373 CAGGGCAACCTGAGCGACTGTGGGCTTCCGGACCCAGTGAAGGGCCAGTTACCACCGGGAC 432

Qy   427 CATGGGTGGATCTCGGGGAGGGCTGCAGCGACAAATGTGGGAATTTGGGGAAAGGATCTCCAAA 486
Db   433 GAGGGCTGGAAGTGGGGTGGCTTCTCGCCGCACATCCGGTCTTCGCCGAAG 492

Qy   487 CTTCTTTGTGGACAGTTTGGGAGAGAGGGGAAGGGATGCCAGAGCCCTGATGAATCTTCACCAAC 546
Db   493 GTCTTGTTGGATGCCCCGGGAGAGTCAAGCACGAAATGCCCGGGACTCTCATGACTTGCACAAC 552

Qy   547 AACAGGGCCGGCCAGTGAGGCCACCATCGAAAAGGACATGCAAATGTCATGGC 606
Db   553 AACGAGGCAGGGCCCGAAAGATCCTGAGAGGAACAATGAAGGCAAGGCCAGTTAAAGTGCCACGGC 612

Qy   607 ATCTCTGGGAGCTGCAGCATACAGACTACGAGACTGCTGGCTGGCTGAAATTCCGGGAGATG 666
Db   613 GTGTCAGGCTCGTGCACCACCAAGACTGCTGGACCACAGTTTGCTGCGGGGAGCTG 672

Qy   667 GGAGACTACCTAAAGCCCAAGTATATGACCAAGGCGCTGAAAATTGAAAATGGATAAGCGGCAG 726
Db   673 GGCTACGTGCTCAAGGACAAGAGTACAACGAGGCCGGTTCACGTGGACCTGTCCAGC 732

Qy   727 CTGAGAGCTGGGGAACAGCGCCGGAGGGGCCACTGGGGTGCCCGCTGAGGGCCTTCCTTCCTAGC 786
Db   733 CGCCACAAGCGGCCCACCTTCCTGAAGATCAAGGAAGCCACTGTCGTGACCGAAGCCCATG 792

Qy   787 GCAGAGACGGGGAAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAAATTCCAGC 846
Db   793 ---GACACGGACCTGGTGTACATCGAGAAGTGCGCCCAACTACTGCGGGAGGGGACCCGGGTG 849

Qy   847 CTGGGGCATCTATGGCACAGAGAGGGTCCGTGAGTGCCTACAGAACAGCCACAACACATCCAGG 906
Db   850 ACCGGCAGTGTGGGCACCCAGGGCGCCGCGCCCTGCAACAAGAAGACGGCTCCCAGGCCAGG 909

Qy   907 TGGGAGCGACGTAGCTGTTGGGCG 929
Db   910 TGTGACCTCATGTGCTGTGGGGCG 932

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 23:32:06 ; Search time 2283 Seconds
                     (without alignments)
                     11816.894 Million cell updates/sec

Title: US-09-898-456-6
Perfect score: 1110
Sequence: 1 atgctgtgctgcattcagtg........tgggtaagggcagtgcctga 1110
Scoring table: IDENTITY NUC
                     Gapop 10.0 , Gapext 1.0
Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Post-processing: Minimum Match 0%
                 Maximum Match 100%
Maximum DB seq length: 200000000
Minimum DB seq length: 0
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_hc:*
                 9: em_hc1:*
          c   10: gb_est1:*
                11: gb_est2:*
                12: gb_est3:*
                13: gb_est4:*
          c   14: gb_est5:*
                15: em_estfun:*
                16: em_estom:*
                17: em_estfun:*
                18: em_gss_hum:*
                19: em_gss_inv:*
                20: em_gss_pln:*
                21: em_gss_vr1:*
                22: em_gss_fun:*
                23: em_gss_mam:*
                24: em_gss_mus:*
                25: em_gss_pro:*
                26: em_gss_rod:*
                27: em_gss_phg:*
                28: em_gss_vr1:*
                29: gb_gss1:*
                     gb_gss2:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result   %   Query
No.   Score Match Length DB ID   Description
----- ----- ----- ------ -- --   -----------
 1   477.2   43.0   3151 11 BC044143   Danio rer
 2   473.6   42.0   825 28 AQ746299   HS_2277_A
 3   431.4   38.9   1915 11 AK050992   Mus muscu
 4   389.6   35.1   685   9 AL651356   AL651356 AL651356

	Score	DB	ID
5	350.4	31.6	665	9	AL652607	AL652607 AL652607
6	349.8	31.5	680	9	AL631116	AL631116 AL631116
7	323.8	29.2	906	14	CD052976	CD052976 LITH2F000
8	316	28.5	924	14	CA790400	CA790400 AGENCOURT
9	299.6	27.0	825	13	BQ770501	BQ770501 UI-M-F10-
10	299.4	27.0	611	9	AL672366	AL672366 AL672366
11	284.2	25.6	778	13	BU261855	BU261855 603520218
12	283.6	25.5	879	14	CD053342	CD053342 LITH2F000
13	267.8	24.1	690	12	BI891257	BI891257 ZF637-3-0
14	266.6	24.0	904	14	CD052815	CD052815 LITH2F000
15	263.4	23.7	743	13	BQ770514	BQ770514 UI-M-F10-
16	262.8	23.7	568	9	AW133833	AW133833 fi12d03.y
17	259.2	23.4	503	9	AW460434	AW460434 da36d12.y
18	258.4	23.3	531	12	BG816071	BG816071 dac07a08.
19	258	23.2	623	12	BI888991	BI888991 ZF637-2-0
20	255	23.0	697	12	BB655336	BB655336 BB655336
21	246.4	22.2	697	9	AL594545	AL594545 AL594545
22	242	21.8	497	9	AL794001	AL794001 AL794001
c 23	237.8	21.4	792	9	AW116191	AW116191 fi12d03.x
c 24	236	21.3	766	9	AW019457	AW019457 fe1lh03.x
25	232.4	20.9	482	9	AL792525	AL792525 AL792525
26	232.4	20.9	658	14	BY745575	BY745575 BY745575
27	194.4	17.5	555	12	BM958218	BM958218 fy70g11.y
28	191	17.2	409	10	BE576612	BE576612 dc42f05.y
29	184.4	16.6	340	10	BF048284	BF048284 dc01c08.y
c 30	184	16.6	838	29	CNS04K0E	CNS04K0E Tetraodon
31	181.4	16.3	530	9	AW059338	AW059338 fe1lh03.y
32	180.2	16.2	529	9	AA163895	AA163895 mb52g10.r
33	179.8	16.2	483	10	BF732616	BF732616 nae13b09.
c 34	162	14.6	896	13	BU541891	BU541891 AGENCOURT
35	162	14.6	898	13	BU543397	BU543397 AGENCOURT
36	159.4	14.4	811	12	BM043406	BM043406 603619767
37	158.4	14.3	478	9	AA170920	AA170920 ms54g01.r
38	157.2	14.2	1291	11	AK043014	AK043014 Mus muscu
39	154.4	13.9	725	12	BI885938	BI885938 ZF637-1-0
40	152	13.7	3402	11	AK087499	AK087499 Mus muscu
41	148.4	13.4	756	14	CA320907	CA320907 UI-M-FW0-
42	148.4	13.4	927	13	BQ958457	BQ958457 AGENCOURT
43	148.2	13.4	755	13	BU702745	BU702745 UI-M-FCO-
44	147.6	13.3	775	13	BU613154	BU613154 UI-M-EW0-
45	147.4	13.3	1007	10	BF608129	BF608129 MYL_00114

                              ALIGNMENTS

RESULT 1
BC044143
LOCUS   BC044143   3151 bp   mRNA   linear   HTC 04-MAR-2003
DEFINITION   Danio rerio, clone IMAGE:2600933, mRNA.
ACCESSION   BC044143
VERSION   BC044143.1 GI:28422285
KEYWORDS   HTC
SOURCE   Danio rerio (zebrafish)
  ORGANISM   Danio rerio
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 3151)
AUTHORS   Strausberg,R.
TITLE   Direct Submission
JOURNAL   Submitted (13-JAN-2003) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
                cDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Institute for Systems Biology
                http://www.systemsbiology.org

contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 101 Row: c Column: 3
This clone has the following problem: retained intron.

```
FEATURES             Location/Qualifiers
source
     1..3151
     /organism="Danio rerio"
     /mol_type="mRNA"
     /strain="AB"
     /db_xref="taxon:7955"
     /clone="IMAGE:2600933"
     /tissue_type="Whole body, adult, (one male and one female,
     including unfertilized eggs)"
     /clone_lib="Sugano Kawakami zebrafish DRA"
     /lab_host="DH10B"
     /note="Vector: pME18S-FL3"

BASE COUNT      913 a      637 c      779 g      822 t
ORIGIN
```

Query Match   43.0%;   Score 477.2;   DB 11;   Length 3151;
Best Local Similarity   68.2%;   Pred. No. 1.7e-129;
Matches 662;   Conservative 0;   Mismatches 308;   Indels 0;   Gaps 0;

```
Qy    96 CTGCCCTCACTTTTTCTCTTTTTGTAGGTCACTGACACAATTTCCTGATAAACAGGTCCCAA 155
         ||| ||| |||  |  ||||| |  | |||||||||| | || |||||||||| ||| |||
Db   136 CTGTCACATACTGTCGTCACAGCACATGGTCTCTGTGAATAACTTCCTGATGACAGGACCAAA 195

Qy   156 GGCCTATCTCGATACAACCAGCAGTGTACACAGTGTGGCCCCAGAGTGGCATCGAGAGTG 215
         ||| |||||||  ||||  |||||||||||   |||||  | |||||||||| |||||||
Db   196 GGCTTATCTCGCATACACCAGCAGTGTACAAGCTGGGGGCCTCAGAGTGGCATCGAGAGTG 255

Qy   216 CAAGTTCCAGTTTGCTTGGGAACGGCTGGAACTGCCCCTGAAAATGCTCTTCAGCTCTCCAC 275
         |||| ||||||||||| |||||| |||||| |||||||||||| |||||| |||||| |||
Db   256 CAAGCCATCAGTTCGCATGGGACACAGGTGGAACTGCCCCCGGAAACGCCACTGCAGTTATCGAC 315

Qy   276 CCACACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTCATTACATCCTATCAGCTCTGC 335
         ||| |||||||||||||| |  ||||||| |||| | | | |  |||||||||| |||
Db   316 GCATAAAGGCCTCGGAGGTGCCACCAGAGAACCGCCCTTTGTCCATGCTATAAGTGCTGC 375

Qy   336 TGGGAGTCATGTACATCATCACCAAGAACTGTAGCCATGGGAGGTGACTTCGAAAAACTGTGTGGCTG 395
         ||||||||||| ||||  ||| ||||| |||||| ||||| || |||||| |||||| ||||||||
Db   376 TGGAGTTATGTACACTTTGACGAAAAACTGCAGCATGGGGGACTTCGAAAAACTGTGTTAAAGC 435

Qy   396 TGATGGGTCAAACAATGGAAAAACACGAGAGGAGGCCATGGGCTGGGGGAGGCCTGCAGGCGA 455
         |||  |||||| |||| |||||| ||| || || |||| | |||||  ||||| | || |||
Db   436 TGACGACTCCAAGATCGGAAAAATGGGGTGGCTCTTCGTCGGGTTGGGGGAGGTTGCAGTGAA 495

Qy   456 CAAATGTGGAATTTGGGAGGAAAAGGATCTCCAAACTCTTTTGTGGACAGTTTGGGAGAAGGGGAA 515
         ||| |||||  ||  ||||| ||   |||  | |||  | |  || |||  |||| |||| |||
Db   496 CAATGTTAACTTTGGAGAGACAGAATTGCTAAACTATTTTGTAAGCATCAAGCATGATCA 555

Qy   516 GGATGCCAGAGCCCTGATGAATCTTCACACAACAACAGGCCCGAGACTGGCAGTGAGAGC 575
         ||| | |||| ||||| |||| ||||||| |||| ||||||||||||||||||||||||
Db   556 CGACTCTCGCGCGCGCGCTCACCTGCATAACAACAGAAGCGCTTGCTGCGTGTTAAAGC 615

Qy   576 CACCATGAAAAGGACATCCAAAATGTCATGGCCATCTCTGGGAGTCGCAGCATACAGACATG 635
         ||| |||| ||| ||| ||  || |||| ||| ||||  |||||||| ||| | || |||
Db   616 AACGCTCAAAAGGAACTTGTAAGTGTCATGGTTTCATGGTTTGTCTGGGAGCTGTAGTATTCAGACATG 675

Qy   636 CTGGCCTGCAGCTGGCTGGAATTCCGGCGAGGATGGGAGACTACTTAAAGCCAGTAGTGACCA 695
         ||||| ||||| |||||||||| |||||| |||||||| |||| |  |||| |||| |||||
Db   676 CTGGATGCAGCTTGCTGATTTCAGAGATATCGGCTCCTACCTAAAAATCAAGACATGATCA 735

Qy   696 GGCGCTGAAAATTGAAAATGAATAAGCGGCAGTAGAATAAGCGGAAAACAGCGCCGAGGGCCA 755
         ||| ||||| ||||||| ||| ||  |||| |||| ||||||| ||||||| || |||||
Db   736 AGCACGGAAAGTTGGAGATGGAGATAAAAATTCGGATTGAGCGGAAGCGGAGCAGGAGTTGGG 795

Qy   756 CTGGGTCCGCGCTGAGCGCCTTCCTTCCTAGCCGCGAGAGCGGGAACTGACTCTTTTTAGGAGGA 815
         |||| ||| ||||||||| |  ||  || |||| | || || || |||| | |  || |||||
Db   — 
```

```
RESULT 2
AQ746299
LOCUS       AQ746299      825 bp    DNA     linear   GSS 19-JUL-1999
DEFINITION  HS_2277_A2_D06_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2277 Col=12 Row=G, genomic survey
            sequence.
ACCESSION   AQ746299
VERSION     AQ746299.1   GI:5533457
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 825)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 2277  row: G  column: 12
            Seq primer: M13 Reverse
            Class: BAC ends
            High quality sequence stop: 825.
FEATURES             Location/Qualifiers
source
     1..825
     /organism="Homo sapiens"
     /mol_type="genomic DNA"
     /db_xref="taxon:9606"
     /clone="Plate=2277 Col=12 Row=G"
     /sex="male"
     /clone_lib="CIT Approved Human Genomic Sperm Library D"
     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
     E-Coli DH10B"
BASE COUNT   210 a   208 c   207 g   180 t   20 others
ORIGIN
```

Query Match   42.7%;   Score 473.6;   DB 28;   Length 825;
Best Local Similarity   95.5%;   Pred. No. 1.1e-128;

```
Db   796 TGGCGCAATAGCGGACACGTTCAGCGAGGTTGCGCGCGACCAGAGAACTCATTTTTATGGAAGA 855
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   816 ATCACCCAGATTACTGTACCTGCAAATTCCAGCCTGGGCATCTATGGCCACAGAGGGTCCTGA 875

Db   856 TTCACCCTGATTACTGCGTGAAAAAACCCTCAGCCATGCCGCCTACAGGCACCAGGAGGA 915
         ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   876 GTGCCTACAGAACCAGCCACCAACAACATCCAGGTGGGGACGGACGTGAGGTTGGGGGCGCTG 935

Db   916 ATGTCTACAACCAGGGGAAGAAATCTTTCTCAAATGGGAGAAGAAGACGTTAGCTGTGGGGCCTGG 975
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   936 CACTGAGTGTGGCTGCAGGTGGAGAGACGAAGAGGAAAACTGAGGTCATGAACCAGCTGTAACTG 995

Db   976 CCACGAAGTGTGGCCCTGAAAAGTAGAGAGAGGATTGAGACAGTGAGCAGTTGTAACTG 1035
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   996 CAAATTCCAAGTGTGGTGTCTGTTACGGTCCTGTCAAGTGTGACCAGTGGTGAGCCAGTA 1055

Db  1036 TAAAATTTCACTGGTTGCTGCCACAGTGTCAAATGCCGAAACATGGAAACAACCGTTACCAGGTA 1095
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1056 TTACTGCGCA 1065
         ||||||||||
Db  1096 TTTTTGCGCA 1105
```

GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 01:04:01 ; Search time 457 seconds
                                     (without alignments)
                                     8852.205 Million cell updates/sec

Title:
Perfect Score: 1110
Sequence: US-09-898-456-6
Sequence: 1 atgctgctgccatcaagtg.............tgggtaagggcagtgctga 1110

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2434939 seqs, 182278265 residues

Total number of hits satisfying chosen parameters: 4869878

Post-processing: Minimum Match 0%
Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000
                      Listing first 45 summaries

Database :   Published Applications NA:*
          1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
          2: /cgn2_6/ptodata/1/pubpna/US07_PCT_NEW_PUB.seq:*
          3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
          4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
          5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
          6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
          7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
          8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
          9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
         10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
         11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
         12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
         13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB2:*
         14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
         15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
         16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
         17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
         18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	989.6	89.2	1650	13	US-10-275-115-1	Sequence 1, Appli
2	988	89.0	1064	11	US-09-842-758-7	Sequence 7, Appli
3	974	87.1	1597	13	US-10-285-976-24	Sequence 24, Appli
4	969.4	87.3	1245	14	US-10-005-947-1	Sequence 3, Appli
5	708.4	63.8	1245	14	US-10-005-947-3	Sequence 3, Appli
6	547	49.3	600	13	US-10-029-386-8756	Sequence 8756, Ap
7	546	49.2	546	13	US-10-029-386-22482	Sequence 22482, A
8	434.6	39.2	2117	13	US-10-285-976-26	Sequence 26, Appli
9	170	15.3	1068	13	US-10-004-113-42	Sequence 42, Appli
10	170	15.3	1195	13	US-10-004-113-41	Sequence 41, Appli
11	170	15.3	1506	13	US-10-285-976-8	Sequence 8, Appli
12	164.4	14.8	2250	13	US-10-285-976-22	Sequence 22, Appli
13	162.8	14.7	1070	13	US-10-305-810-1	Sequence 1, Appli
14	162.6	14.6	1082	13	US-09-954-342-1	Sequence 1, Appli
15	162.6	14.6	1116	13	US-09-954-342-3	Sequence 3, Appli
16	162.6	14.6	2932	13	US-10-285-976-10	Sequence 10, Appl
17	157.2	14.2	1068	13	US-10-004-113-39	Sequence 39, Appl
18	157.2	14.2	3000	13	US-10-004-113-38	Sequence 38, Appl
19	149.4	13.5	966	12	US-10-028-248A-17	Sequence 17, Appl
20	149.4	13.5	1050	9	US-09-903-817-1	Sequence 1, Appl
21	149.4	13.5	1736	12	US-10-295-027-1124	Sequence 1124, Ap
22	149.4	13.5	1736	13	US-10-285-976-20	Sequence 20, Appl
23	145.8	13.1	1628	12	US-10-028-248A-15	Sequence 15, Appl
24	133	12.0	1108	9	US-09-764-903-29	Sequence 29, Appl
25	133	12.0	1108	15	US-10-091-391-14	Sequence 14, Appl
26	132.4	11.9	1107	9	US-09-764-903-23	Sequence 23, Appl
27	132.4	11.9	1107	15	US-10-091-391-29	Sequence 29, Appl
28	129.2	11.6	1198	13	US-10-285-976-12	Sequence 12, Appl
29	129.2	11.6	1515	14	US-10-002-600-54	Sequence 54, Appl
30	129.2	11.6	1598	14	US-10-098-841-251	Sequence 251, App
31	128.8	11.6	1202	9	US-09-764-903-28	Sequence 28, Appl
32	128.8	11.6	1202	15	US-10-091-391-28	Sequence 28, Appl
33	128.2	11.5	2251	13	US-10-285-976-16	Sequence 16, Appl
34	128.2	11.5	2252	12	US-10-295-027-583	Sequence 583, App
35	127.6	11.5	2049	10	US-09-978-295A-225	Sequence 225, App
36	127.6	11.5	2049	10	US-09-978-697-225	Sequence 225, App
37	127.6	11.5	2049	13	US-10-285-976-14	Sequence 14, Appl
38	127.6	11.5	2049	15	US-10-091-391-28	Sequence 16, Appl
39	127.6	11.5	2049	10	US-09-978-189-225	Sequence 225, App
40	127.6	11.5	2049	10	US-09-978-608A-225	Sequence 225, App
41	127.6	11.5	2049	11	US-09-978-585A-225	Sequence 225, App
42	127.6	11.5	2049	10	US-09-978-192A-225	Sequence 225, App
43	127.6	11.5	2049	11	US-09-978-403A-225	Sequence 225, App
44	127.6	11.5	2049	11	US-09-978-564A-225	Sequence 225, App
45	127.6	11.5	2049	11	US-09-999-833A-225	Sequence 225, App

ALIGNMENTS

RESULT 1
US-10-275-115-1
; Sequence 1, Application US/10275115
; Publication No. US20030175805A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New wingless gene Wnt-8D
; FILE REFERENCE: WNT8dKDWS
; CURRENT APPLICATION NUMBER: US/10/275,115
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)..(1155)
US-10-275-115-1

Query Match 89.2%; Score 989.6; DB 13; Length 1650;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 992; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy   115 TTTGTTAGGTCAGTGAACAATTTTCTTGATAACAGTTCCCAAGGCCTPATCTGACCTACACG 174
         ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   160 TCTGCCTGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTPATCTGACCTACACG 219

Qy   175 ACTAGTGTGGCGCCTTGGGTGCGTGCCCAGAGTGGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   175 ACTAGTGTGGCGCCTTGGGTGCGTGCCCAGAGTGGGCATCGAGGAGTGCAAGTTCCAGTTTTGCTTGG 234

Db   220 ACTAGTGTGGCCCTTGGGTGCCCAGAGTGGCCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 279

Qy   235 GAACGCTGGAACTGCCCTGAAAATGCTCTTCAGCTCTTCACCCACAACACAGGCTGAGAAGT 294
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   280 GAACGCTGGAACTGCCCTGAAAAATGCTCTTCAGCTCTTCCACCCACAACACAGGCTGAGAAGT 339

Qy   295 GCTACCAGAGAGACTTCCTTCATACAATGCTATCAGTCTCGTCTGGAGTCATGTACATCATC 354

RESULT 2
US-09-842-758-7
Sequence 7, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Esha A
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: Macdougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US2003008324441el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 7
; LENGTH: 1064
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-842-758-7

Query Match 89.0%; Score 988; DB 11; Length 1064;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 991; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy  340 GCTACCAGAGAGAGACATTCCTTCATACATGCTATCAGCTCTCCTCTGGAGTCAATGTACATCATC 399
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  355 ACCAAGAACTGTAGCAGAGACTTCCTTCATACATGGGTGACTTCGAAAACTGGGTCGTGGATCAGGAACAAT   414

Qy  115 TTTGGTAGGTCAGTGAACACAATTTCCTGATAAACAGGTCCCAAGGCCTTATCTGACCTACACG 174
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 TCTGCCTGGTCAGTGAACAATTTCCTGATAAACAGGTCCCAAGGCCTTATCTGACCTACACG   123
```

RESULT 3
US-10-285-976-24

; Sequence 24, Application US/10285976
; Publication No. US20030165500A1
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Wu, Christina
; APPLICANT: Malini, Sen
; APPLICANT: Leoni, Lorenzo M.
; APPLICANT: Corr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
; TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
; FILE REFERENCE: 023070-13032US
; CURRENT APPLICATION NUMBER: US/10/285,976
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24

; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wnt-8a
US-10-285-976-24

Query Match   87.7%;   Score 974;   DB 13;   Length 1597;
Best Local Similarity   99.5%;   Pred. No. 0;
Matches 977;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;

[Sequence alignment — Qy (query) vs Db (database), DNA nucleotide sequences with match bars between paired lines and residue position numbers flanking each line.]

```
Db  1061 ACGGTCAAGTGTGACCAGTGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCA 1120
Qy  1075 GGCAGTGCCCAGTCCCTGGGTA 1096
Db  1121 GGCAGTGCCCAGTCCCTGGGGA 1142
```

RESULT 4
US-10-005-947-1
; Sequence 1, Application US/10005947
; Publication No. US20020123103A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; TITLE OF INVENTION: Human Wnt Gene
; FILE REFERENCE: 99-87
; CURRENT APPLICATION NUMBER: US/10/005,947
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: US/09/715,993
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1245)
US-10-005-947-1

Query Match   87.3%;   Score 969.4;   DB 14;   Length 1245;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 973;   Conservative 0;   Mismatches 6;   Indels 0;   Gaps 0;

```
Qy  115 TTTGGTTAGGTTCAGTGAACAATTTCCTGATAACAGGTCCCAAGCGCTTATCCTGACCTACACG 174
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TCTGCCTTGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGCGCTTATCCTGACCTACACG 120

Qy  175 ACTAGTGTGCCCTTGGGTGCGCCAGAGTGGCATCGGAGGAGTGCAAGTTCCAGTTTGCTTGG 234
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 ACTAGTGTGCCCTTGGGTGCCCAGAGTGGCATCGGAGGAGTGCAAGTTCCAGTTTGCTTGG 180

Qy  235 GAACGCTGGGAACTGCCCTGAAAAATGCTTCTTCAGCTTCAGCTGCAGCGCTGAGAAGT 294
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 GAACGCTGGGAACTGCCCTGAAAAATGCTCTTCCAGCTTCCACCCACAACAGGCGCTGAGAAGT 240

Qy  295 GCTACCAGAGAGACTTCCTTCATACATGTCTATCAGCTCTCCTGCTGGAGTCATGTCAATCATC 354
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GCTACCAGAGAGACTTCCTTCATACATGTCTATCACTCTCCTGGAGTCATGTCAATCATC 300

Qy  355 ACCAAGAACTGTAGCATGGGGTGACTTCGAAAACTGTGGGGTCTGATGGGTCAAACAATGGA 414
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 ACCAAGAACTGTAGCATGGGTGACTTCGAAAAACTGTGGGGTCTGATGGGTCAAACAATGGA 360

Qy  415 AAAACAGGAGGCAGGCCATGGCCTGGATCTCGGGGAGGCTCGGGGAGGTGTGGAATTTGGGGAA 474
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 AAAACAGGAGGCCATGGCCTGGATCTCGGGGAGGCTCGGGGAGGTGTGGAATTTGGGGAA 420

Qy  475 AGGATCTCCAAACTCTTTGTTGGACAGTTTGGAGAAGGGGAAGGGGATGCCAGAGCCCTGATG 534
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 AGGATCTCCAAACTCTTTGTTGGACAGTTTGGAGAAGGGGAAGGGGATGCCAGAGCCCTGATG 480

Qy  535 AATCTTCACAACACAGGGCCGGCGGCCAGAGACTGGGCATGGCCACCACCATGAAGGACATGC 594
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 AATCTTCACAACACAGGGCCGGCGGCCAGAGACTGGTCGTGAGAGGCCACCATGAAGGACATGC 540

Qy  595 AAAATGTCATGGCATCTCTGGGAGCTGCAGCATACAGACAGAGACTGCGCTGCGAGCTGAA 654
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AAAATGTCATGGCATCTCTGGGAGCTGCAGCATACAGACAGAGACTGCGCTGCGAGCTGAA 600

Qy  655 TTCCGGGGAGATGGGAGACTACCTAAAGGCCAAGTGTAGACCAGGCCCTGAAAAATTGAAATG 714
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 TTCCGGGGAGATGGGAGACTACCTAAAGGCCAAGTGTAGACCAGGCCCTGAAAAATTGAAATG 660
```

```
Qy  715 GATAAGCGGCAGCTGAGAGCTGGGAGACAGCGCGCAGCGGCCACTGGGTGCCGGCTGCCGGAGGCC 774
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 GATAAGCGGCAGCTGAGAGCTGGGAGACAGCGCGCAGCGGCCACTGGGTGCCGGCTGCCGGAGGCC 720

Qy  775 TTCCTTCCTTAGCGCGCAGAGGGGGGAGGGGAACCGGGTCCACTGTCTTTTTGAGAGGAATCACCAGATTACTGTACC 834
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TTCAATTCCAGCCTGCACAGAGGGGGCATCTATGCCACAGAGGTCGTTGCCTTACGAGACAGGAAC 780

Qy  835 TGCAATTCCAGCCTGGGCATCTATGCCACAGAGGTCGTTGCCTTACGAGACAGGAAC 894
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TGCAATTCCAGCCTGGGCATCTATGCCACAGAGGTCGTTGCCTTACGAGACAGGAAC 840

Qy  895 AACACATCCAGGTGGAGGCGGACGTACCTGTGGGGCGCCTGTGCCACTGAGTGTGGGCTGCAG 954
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 AACACATCCAGGTGGGGAGCCGACGTACCTGTGGGGCGCCTGTGCCACTGAGTGTGGGCTGCAG 900

Qy  955 GTGGAAGAGAGGAGAAAACTGAGGTCATAAGCAGCTCAAACTGCACTCAGTGGTGCTGTGT 1014
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GTGGAAGAGAGGAGAAAACTGAGGTCATAAGCAGCTCAAACTGCACTCAGTGGTGCTGTGT 960

Qy 1015 ACGGTCAAGTGTGACCAGTGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCA 1074
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 ACGGTCAAGTGTGACCAGTGTGTAGGCATGTGGTGAGCAAGTATTACTGCGCACGCTCCCA 1020

Qy 1075 GGCAGTGCCCAGTCCCTGG 1093
        |||||||||||||||||||
Db 1021 GGCAGTGCCCAGTCCCTGG 1039
```

RESULT 5
US-10-005-947-3
; Sequence 3, Application US/10005947
; Publication No. US20020123103A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; TITLE OF INVENTION: Human Wnt Gene
; FILE REFERENCE: 99-87
; CURRENT APPLICATION NUMBER: US/10/005,947
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: US/09/715,993
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate sequence encodes the amino acid
; FEATURE:
; OTHER INFORMATION: sequence of SEQ ID NO:2.
; NAME/KEY: variation
; LOCATION: (1)...(1245)
; OTHER INFORMATION: N is any nucleotide.
US-10-005-947-3

Query Match   63.8%;   Score 708.4;   DB 14;   Length 1245;
Best Local Similarity   56.5%;   Pred. No. 2.7e-234;
Matches 564;   Conservative 258;   Mismatches 176;   Indels 0;   Gaps 0;

```
Qy   96 CTGCCTCACTTTTTCTCTTTTTGGTAGGTCAGTGAACAATTTCCTGATAACAGGTCCCAA 155
        |||||:.|..|:|:||||||||||||||||||:||||:||||||||||||||||:|.|:
Db   42 YTGYGCNGCNTTYWSNGCNTTYGGWSNGNTGGWSNGTNAAYAAYTTYYTNATHACNGNGNCCNAA 101

Qy  156 GGCCTATCTGACCTACACGACTAGTGTGCCCTTGGGTGCCCAGAGTGGCATCGGAGGAGTG 215
        ||.:||:|:|||.|:|||:||||:|.:||:||||||:|||:||||:||||||:|.:|||:
Db  102 RGCNTAYYTNACNTAYACNACNWSNGTNCCNYTNGGNGCNCARWSNGGNATHGARGARTG 161

Qy  216 CAAGTTCCAGTTTGCTTGGGGAACGCTGGGAACTGCCCTGAAAAATGCTCTTCAGCTCTCCAC 275
        |||:||.|||:||:|||||||||.:||||||:|||.|:||||||.:||.||:|||.|:|||:||:
Db  162 YAARTTYCARTTYGCNTGGGGNARMGNTGGGAAYTGYCCNGARAAAYGCNYTNCARYTNWSNAC 221

Qy  276 CCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTCTGC 335
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  276 CCACAACAGGCTGAGAAGTGCTACCAGAGAGACTTCCTTCATACATGCTATCAGCTCTCTGC 335
```

```
Qy  222  NCAYAAYMGNYTNMGNSNGCNACNMGNGNARAACNWSNTTYATHCAYGCNATHWSNWSNGC  ||
Db  281

Qy  336  TGGAGTCAYTGTACNTCATCACCAAGAACTGTAGCATGGGGTTGACTTCGAAAACTGTGGCTG  395
Db  282  NGGNGTNAGTCNAYATHATHACNAARAAYTGYWSNATGGGNGAYTTYGARAAYTGYGGNTG  341

Qy  396  TGATGGGTCAAACAATGGAAAAACAGGAGGCCATGGCTGATCTCTGGGAGCCTGCAGCGA  455
Db  342  YGAYGGNWSNAAAYAAYGGNAARACNGGNGGNCAYGGNNTGGAITHGGGNGGNGNTGYWSNGA  401

Qy  456  CAAATGTGGAATTTGGGGAAAGGATCTCCAAAACTCTTTGTGGGACAGTTTGGAGAGAAGGGAA  515
Db  402  YAAYGTNGARTTYGGNGARTTYGGNGARMGNATHWSNAARYTNTTYGTNGAYWSNNYTNGARARAGGNAA  461

Qy  516  GGATCCAGAGCCCTGATGAATCTTCACAACAACAGGGCCGGCAGACTGGCAGTGAGAGC  575
Db  462  RGAYGCNMGNGCNYTNATGAAYTNCAYAAYAAYMGNGCNGGNGARAAYTGGNGCNGNYTNMGNGNC  521

Qy  576  CACCATGAAAAGGACATGCAAAATGTCATGGCATCTCAGCATACAGACATG  635
Db  522  NACNATNGAARMGNACNTGYAARTGYCAYGGNATHWSNGGNWSNATHCARACNTG  581

Qy  636  CTGGCTGCAGCTGGCCTGAATTCCGGGAGAGGAGACTACCTAAAGGCCAAGTATGACCA  695
Db  582  YTGGCYTNCARYTNGCNGARTTYMGNGARATGGGNGAYTAYTNAARGCNAARTAYGAYCA  641

Qy  696  GGGGCTGAAAATTGAAAATGGATTAACGGGCAGCTGAGAGTTTNAARGCNAARTAYGAYCA  755
Db  642  RGCNYTNAARATHGARATGGAYAARMGNCARYTNMGNGCNAGYAARYWSNGCNGARGGNCA  701

Qy  756  CTGGGGTGCCCGCTGAGGGCCTTCCTTCCTAGGCGCGAGAGGCGGAACTGATCTCTTTTAGAGGA  815
Db  702  YTGGGGTNCNGGNCNGARGRCNTTYYTNCCNWSNGCNGARGGNCNATCTCNTGATHTTYYTNGARGA  761

Qy  816  ATCACCAGATTACTGTTACCTGCCAATTCCAGCCTGGGCCATCTATGGCCACAGAGGGTCGTCTGA  875
Db  762  RWSNCCNGAYTAYTGYACNTGYAAYWSNWSNYTNGGNATHTAYGGNCACAGRGGNWSNGNGA  821

Qy  876  GTGCCTACAGAACACCACACAACATCCAGTGTGGGAGCGAGCGTACCTGTGGGCGCGCCTGTG  935
Db  822  RTGYYTNCARAAYWSNCAYAAYACNWSNMGNTGYGGNRMGNWSNTGYGNNNYTNTG  881

Qy  936  CACTGAGTGTGTGGGGCTGCAGGTGGAGAGAGGAGGAAAAACTGCTGCAGCGTAAACTG  995
Db  882  YACNGARYGYGGNYTNCARGTNGARGGARMGNAAAACNGNGARGTNAATHWSNWSNSNTGYAAAYTG  941

Qy  996  CAAATTCCAGTGGTGCTGCTTACGGGTCAAGTGTGCCAGTGTAGGCCATTGTGGTCGCAAGTA  1055
Db  942  YAARTTYCARTGGTGYTGYACNGTNAARTGYGAYCANGTNAAYWSNAARTA  1001

Qy  1056  TTACTGCGCACGCTCCCCAGGCAGTGCCCAGTCCCTGG  1093
Db  1002  YTAYTGYGCNMGNWSNCCNGGNWSNGCNCARWSNYTNG  1039
```

```
Query Match             49.3%;  Score 547;  DB 13;  Length 600;
Best Local Similarity   100.0%;  Pred. No. 1.7e-178;
Matches 547;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  564  GGCAGTGAGAGCCACCATGAAAAGGACATGCAAAATGTCATGGCATCTCTGGGAGCCTGCAG  623
Db   29  GGCAGTGAGAGCCACCATGAAAAGGACATGCAAAATGTCATGGCATCTCTGGGAGCCTGCAG   88

Qy  624  CATACAGACATGCTGCAGCTGCAGCTGGCCTGAATTCCGGGAGGATGGGAGGACTACCTAAAGGC  683
Db   89  CATACAGACATGCTGCAGCTGGCCTGAATTCCGGGAGGATGGGAGGACTACCTAAAGGC  148

Qy  684  CAAGTATGACCAGGGGCGCGGTGAAAATTGAAAATGGATTAAGCGGCGAGCTGAGAGTTTGGAACAG  743
Db  149  CAAGTATGACCAGGGGCGCGGTGAAAATTGAAAATGGATTAAGCGGCGAGCTGAGAGTTTGGAACAG  208

Qy  744  CGCCGAGGGCCACTGGGGTGCCCGCTGAGGGCCTTCCTTCCTAGGCGCGAGAGGCGGAACTGAT  803
Db  209  CGCCGAGGGCCACTGGGGTGCCCGCTGAGGGCCTTCCTTCCTAGGCGCGAGAGGCGGAACTGAT  268

Qy  804  CTTTTAGAGGAATCACCAGATTACTGTTACCTGCCAATTCCAGCCTGGGCCATCTATGGCCAC  863
Db  269  CTTTTAGAGGAATCACCAGATTACTGTTACCTGCCAATTCCAGCCTGGGCCATCTATGGCCAC  328

Qy  864  AGAGGGTCGTCTGAGTGCCTACAGAACAGCCACACAACATCCAGTGTGGGAGCGAGCGTACCTG  923
Db  329  AGAGGGTCGTCTGAGTGCCTACAGAACAGCCACACAACATCCAGTGTGGGAGCGAGCGTACCTG  388

Qy  924  TGGGCGCGCCTGTGCACTGAGTGTGTGGGGCTGCAGGTGGAGAGAGGAGGAAAAACTGAGGTCATAAG  983
Db  389  TGGGCGCGCCTGTGCACTGAGTGTGTGGGGCTGCAGGTGGAGAGAGGAGGAAAAACTGAGGTCATAAG  448

Qy  984  CAGCTGTAACTGCAAAATTCCAGTGGTGCTGCTTACGGGTCAAGTGTGCCAGTGTAGGCCATGT  1043
Db  449  CAGCTGTAACTGCAAAATTCCAGTGGTGCTGCTTACGGGTCAAGTGTGCCAGTGTAGGCCATGT  508

Qy  1044  GGTGAGCAAGTATTACTGCGCACGCTCCCCAGGCAGTGCCCAGTCCCTGGGTAAGGGCAG  1103
Db  509  GGTGAGCAAGTATTACTGCGCACGCTCCCCAGGCAGTGCCCAGTCCCTGGGTAAGGGCAG  568

Qy  1104  TGCCTGA  1110
Db  569  TGCCTGA  575
```

;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION:
;   OTHER INFORMATION: MAP TO AC004826.3
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.61
;   OTHER INFORMATION: EST_HUMAN HIT: AI741277.1, EVALUE 1.20e-02
;   OTHER INFORMATION: SWISSPROT HIT: Q9HJJ5, EVALUE 1.00e-107
;   OTHER INFORMATION: NT HIT: gi1478158, EVALUE 0.00e+00
US-10-029-386-22482

Query Match   49.2%; Score 546; DB 13; Length 546;
Best Local Similarity   100.0%; Pred. No. 3.6e-178;
Matches 546; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   565 GCAGTGGAGAGCCACCATGAAAAAGGACATGCAAAATGTCATGGCATCTCTCTGGGAGCTGGCAGC 624
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCAGTGGAGAGCCACCATGAAAAAGGACATGCAAAATGTCATGGCATCTCTCTGGGAGCTGCAGC 60

Qy   61 ATACAGACATGCTGGCGTGCAGCTGGCTGGCTGAATTCCGGGAGAGATGGGAGACTACCTAAAGGCC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATACAGACATGCTGGCGTGCAGCTGGCTGGCTGAATTCCGGGAGAGATGGGAGACTACCTAAAGGCC 684

Qy   625 ATACAGACATGCTGGCGTGCAGCTGGCTGGCTGAATTCCGGGAGAGATGGGAGACTACCTAAAGGCC 684

Qy   685 AAGTATGACCAGGCGCGCTGAAAAATTGAAAATGGATAAGCGGCACTGAGACTGAGGAGGAACAGC 744
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAGTATGACCAGGCGCGCTGAAAAATTGAAAATGGATAAGCGGCACTGAGACTGAGGAGGAACAGC 180

Qy   745 GCCGAGGGCCACTGGGGTGCCCGCTGAGGCGTTCCTTCCTTAGCGCACAGAGGCCGAACTGATC 804
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCCGAGGGCCACTGGGGTGCCCGCTGAGGCGTTCCTTCCTTAGCGCACAGAGGCCGAACTGATC 240

Qy   805 TTTTTAGAGGAATCACCAGATTACTGTACCTGGGCATCTCATCTATGGCACA 864
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTTTTAGAGGAATCACCAGATTACTGTACCTGGGCATCTCATCTATGGCACA 300

Qy   865 GAGGGTCGTGAGTGCCTACAGAACAGCAACACCATCCAGGTGGGGAGGCGAACTAGCTGT 924
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GAGGGTCGTGAGTGCCTACAGAACAGCAACACCATCCAGGTGGGGAGGCGAACTAGCTGT 360

Qy   925 GGGGCGCCTGTCACTCAGTGTGGTGGGGCTCCAGGTGGAAGAGAGGAAAAACTGAGGTCATAAGC 984
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GGGGCGCCTGTCACTCAGTGTGGTGGGGCTCCAGGTGGAAGAGAGGAAAAACTGAGGTCATAAGC 420

Qy   985 AGCTGTAACTCGCAAATTCCAGTGGTGGCTGCTGTACGGTCAAGTGTTAGGTTGTAGGTTGAGGTTCATTAAGC 1044
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGCTGTAACTCGCAAATTCCAGTGGTGGCTGCTGTACGGTCAAGTGTTAGGTTGTAGGTTGAGGTTCATTAAGC 480

Qy   1045 GTGAGCAAGTATTACTTCGGCACGCTCCCCAGGCAGTGCCCAGTCCCTGTGGGTTAAGGGCCAGT 1104
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGAGCAAGTATTACTTCGGCACGCTCCCCAGGCAGTGCCCAGTCCCTGTGGGTTAAGGGCCAGT 540

Qy   1105 GCCTGA 1110
           ||||||
Db   541 GCCTGA 546

RESULT 8
US-10-285-976-26
;   Sequence 26, Application US/10285976
;   Publication No. US20030165500A1
;   GENERAL INFORMATION:
;   APPLICANT: Rhee, Chae-Seo
;   APPLICANT: Malini, Sen
;   APPLICANT: Wu, Christina
;   APPLICANT: Leoni, Lorenzo M.
;   APPLICANT: Corr, Maripat
;   APPLICANT: Carson, Dennis A.
;   APPLICANT: The Regents of the University of California
;   TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
;   TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
;   FILE REFERENCE: 023070-13032US
;   CURRENT APPLICATION NUMBER: 023070-13032US
;   CURRENT FILING DATE: 2002-11-01

;   PRIOR APPLICATION NUMBER: US 60/287,995
;   PRIOR FILING DATE: 2001-05-01
;   PRIOR APPLICATION NUMBER: WO PCT/US02/13802
;   PRIOR FILING DATE: 2002-05-01
;   NUMBER OF SEQ ID NOS: 232
;   SOFTWARE: Patentin Ver. 2.1
;
SEQ ID NO 26
;   LENGTH: 2117
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human Wnt-8b
US-10-285-976-26

Query Match   39.2%; Score 434.6; DB 13; Length 2117;
Best Local Similarity   67.0%; Pred. No. 3.5e-139;
Matches 636; Conservative 0; Mismatches 304; Indels 9; Gaps 1;

Qy   122 GGTCAGTGAACAAATTTCCTGATAACAGGTCCAAGGGCTATCTGACCTTACGACGACTAGTG 181
           ||||||||||||||||||| |||||||||||||||| |||||||||||| |||||||||||
Db   203 GGTCGGGTGAACAATTTCCTGATGACAGTGGTTCCAAAGGCTTACCTGATTACTTACCAGAGTG 262

Qy   182 TGGCCTTGGGTGTCCCAGAGTGCCATCAGAGGACTGCAAGTTCCAGTTTGCTTGGGAACGGCT 241
           |||| |||||||||| |||||| |||||| |||| || |||| |||||| |||||| |||
Db   263 TGGCAGTGGTGTCCCAGAGTGGTTATTGAAGAACAGCAAGTATCAGTTTGCCTTGGGACCGGCT 322

Qy   242 GGAACTGCGCCCTGAAAAATGCTTTCTTCAGCTCTTCCACCCACAACAGGCTGAGGAAGTGCTACCA 301
           ||||| || |||||||| |||| ||||| |||| |||||||||||||| ||||||||||||||
Db   323 GGAACTGCCCCTGAGAGAGGCCCTGCAGCTGTCCAGCCATGGTGGGCCTTCGCAGTGCCAATC 382

Qy   302 GAGAGACATTCCTTCATACATGCTATCAGCTTCTGCTGAGGCATCATGTACATCACCAAGA 361
           |||||| |||||||||||||| |||| || |||||||||| ||||||| |||||||||
Db   383 GGGGAGACAGCATTTGTTGCATGCTCCCATCAGTTCTGCTGGAGTCATCATGTACACCCTGACTAAGA 442

Qy   362 ACTGTAGCATGGGTGACTTCGAAAAACTGTGGGTCTGATGGGTTCAAACAATGGAAAAACAG 421
           ||||| ||||||| |||||| |||| ||| ||| |||| |||| |||| ||||||||||
Db   443 ACTGCAGCCTTGGAGATTTTGATAACTGTGGAGTCCCTGGGTTCAGGTCAACAGGCAACTGG 502

Qy   422 GAGGCCATGGCTGTGGATCTCTGGGGAGAGGGCTGCACGGCACAAATGGGAAATTGGGGGAAGAGATCT 481
           |||| |||| |||| |||||||||||| |||||||| ||||| |||| |||| |||||||
Db   503 GGGGACAAGGCTGGCTGTGCAGTGACACAATGTGGGCTTCGAGAGGCGATTT 562

Qy   482 CCAAACTCTTTGTTGGACAGTTTGGAGAGGAGAGGGGAAAGGGAGGAGCCCCTGATGAAATCTTC 541
           ||| ||| |||||| ||||||| ||| | |||| ||| ||| |||||||||||| ||| |
Db   563 CCAAGCAGTTTGTTCTGGATGCCTCGGAAAGCAGGAGAGCACGGGCGCAGAGCCCCATGGATGTTC 622

Qy   542 ACAACAACAGAGGCGCGGCAGACTGGGCACTGAGAAACCAGGAAAAGGACATGCAAAATGTC 601
           || || || ||||| |||| || | |||||| |||||| || ||| ||| |||| ||||
Db   623 ACAACAACGAGGGCTGGCCGGAAAGGCCACCATGAAAACGACGTGTTAAGTGCC 682

Qy   602 ATGGCCATCTCTCTGGGAGCTGCAGCATACAGACATGCTCGGGCGCTGGAATTCCGGG 661
           |||| || || |||||||||||| ||||| || ||||| || |||||||||||||
Db   683 ATGGCGGTGTCTCTGGCCAGCGTGCCGAGACCCTGGCTCAGCTCGCCCGAGTTCCCG 742

Qy   662 AGATGGGAGACTACCTAAAAGGCCAAGTATGACCAGGCGCTGAAAAATTGAAAATGGATAAGC 721
           ||| ||||||||| | ||||||||||| |||||| || |||||||| ------GGTGACC 793
Db   743 AGGTTGGGGTGTCTGGCATCAGCTGCACCACAGCCAGCACCTGTTGGCTCAGCTGGCTGGATAAGC
Db   793 ------GGTGACC

Qy   722 GGCAGCTTGAGAGCTTGGGAACACGCCCAGGGGCCACTGGGTGCCCGCTGAGCGCTTTCTTC 781
           |||||||| ||||| ||| |||| |||||||| |||| || |||||||| ||| |||
Db   854 CCATCTCTACCCGGGAGCTGGTGTCACTGGAGGACTCCTGGAACTGCGCCCTGAGCGCTTTCTTC 913

Qy   782 CTAGCGCAGAGGCGGAACTGATCTTTTTAGAGGAATCACCAGATTACTGTACCTGCAATT 841
           ||||| |||||||| |||| || |||| |||||||| ||||| ||| |||| ||| ||||
Db   854 CCATCTCTACCCGGGAGCTGGTGTCACTGGAGGACTCCTGGAACTGCGCCCTGAGCGCTTTCTTC 913

Qy   842 CCAGCCTGGGCCATCTATGGCACAGAGAGGGTTCGTGAGTGCCTACAGAACAGCAACACAT 901
           |||| ||||| ||| | |||||||||| || | |||||||||||||| || |||| |||
Db   914 AAACGCTAGGGGCTGCTGGGCCACCGAAGCGCTTAGGGCGGGCTACAGAGACAACCAACACAT 973

Qy   902 CCAGGTGGGAGCGGACGTAGCTGTGGGGGCCCCTGCACTGAGTGTGGGGCCCTGGAAG 961
           ||||||| ||||| |||||||| |||| ||| ||||||||| ||||| |||||||
Db   974 GTCGCGCTGGGAACTCCGCAGCTCCGCGCTCTGCGGGGGACTGCGCCGGGTGGCGGTGAGG 1033

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 23:55:41 ; Search time 445 Seconds
(without alignments)
7050.754 Million cell updates/sec

Title: US-09-898-456-6
Perfect score: 1110
Sequence: 1 atgctgtgctgcattcagtg...........tgggtaagggcagtgcctga 1110
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4893588 seqs, 141326768 residues

Total number of hits satisfying chosen parameters: 9787176

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	989.6	89.2	1899	1	PCT-US03-37355-57	Sequence 57, Appl
2	986.4	88.9	1056	7	US-10-451-168-11	Sequence 11, Appl
3	170	15.3	1506	1	PCT-US03-37355-53	Sequence 53, Appl
4	164.4	14.8	1047	7	PCT-US03-0418B-1	Sequence 1, Appl
5	164.4	14.8	1047	1	US-10-364-888-1	Sequence 1, Appli
6	164.4	14.8	2160	7	PCT-US03-0418B-7	Sequence 7, Appli
7	164.4	14.8	2160	7	US-10-364-888-7	Sequence 7, Appli
8	162.8	14.7	1070	7	PCT-US03-0418B-5	Sequence 5, Appli
9	162.8	14.7	1070	7	US-10-364-888-5	Sequence 5, Appli
10	162.6	14.6	1002	7	PCT-US03-25100-147	Sequence 147, App
11	162.6	14.6	1002	1	PCT-US03-25100-141	Sequence 141, App
12	162.6	14.6	1014	1	PCT-US03-25100-159	Sequence 159, App
13	162.6	14.6	1056	1	PCT-US03-25100-151	Sequence 151, App
14	162.6	14.6	1059	1	PCT-US02-36071A-60	Sequence 60, Appl
15	162.6	14.6	1060	1	PCT-US03-25100-145	Sequence 145, App
16	162.6	14.6	1060	1	PCT-US03-25100-173	Sequence 173, App
17	162.6	14.6	1060	1	PCT-US03-25100-175	Sequence 175, App
18	162.6	14.6	1071	1	PCT-US03-25100-155	Sequence 155, App
19	162.6	14.6	1076	1	PCT-US03-25100-169	Sequence 169, App
20	162.6	14.6	1081	1	PCT-US03-25100-139	Sequence 139, App
21	162.6	14.6	1081	1	PCT-US03-25100-161	Sequence 161, App
22	162.6	14.6	1082	1	PCT-US03-25100-167	Sequence 167, App
23	162.6	14.6	1099	1	PCT-US03-25100-153	Sequence 153, App
24	162.6	14.6	1116	1	PCT-US03-25100-143	Sequence 143, App
25	162.6	14.6	1116	1	PCT-US03-25100-177	Sequence 177, App
26	162.6	14.6	1116	1	PCT-US03-25100-179	Sequence 179, App
27	162.6	14.6	1116	1	PCT-US03-25100-187	Sequence 187, App
28	162.6	14.6	1116	1	PCT-US03-25100-189	Sequence 189, App
29	162.6	14.6	1116	1	PCT-US03-25100-191	Sequence 191, App
30	162.6	14.6	1555	1	PCT-US02-36071A-59	Sequence 59, Appl
31	162.6	14.6	2932	1	PCT-US02-36071A-57	Sequence 57, Appl
32	162.6	14.6	966	1	PCT-US03-25100-181	Sequence 181, App
33	161	14.5	1116	1	PCT-US03-25100-183	Sequence 183, App
34	161	14.5	1116	1	PCT-US03-25100-185	Sequence 185, App
35	159.4	14.4	1194	1	PCT-US03-25100-165	Sequence 165, App
36	159.4	14.4	1194	1	PCT-US03-25100-171	Sequence 171, App
37	153.4	13.8	2814	1	US-10-454-246-41	Sequence 41, Appl
38	152.6	13.7	849	1	PCT-US03-17512-41	Sequence 41, Appl
39	152.4	13.7	966	6	US-10-454-246-41	Sequence 41, Appl
40	152.4	13.7	1059	1	PCT-US03-25100-149	Sequence 149, App
41	151.4	13.6	966	1	PCT-US02-36071A-57	Sequence 57, Appl
42	151	13.6	966	1	PCT-US03-17512-35	Sequence 35, Appl
43	151	13.6	966	6	US-10-454-246-35	Sequence 35, Appl
44	151	13.6	966	6	US-10-454-246-39	Sequence 39, Appl
45	151	13.6	966	6	US-10-454-246-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
PCT-US03-37355-57
; Sequence 57, Application PC/TUS0337355
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND TISSUE
; TITLE OF INVENTION: REGENERATION
; FILE REFERENCE: HYDR-PW1-004
; CURRENT APPLICATION NUMBER: PCT/US03/37355
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 57
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37355-57

Query Match 89.2%; Score 989.6; DB 1; Length 1899;
Best Local Similarity 99.6%; Pred. No. 2.3e-302;
Matches 992; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy    115 TTTGGTAGGTCAGTGAACAATTTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACG 174
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 TCTGCCCTGGTCAGTGAACAATTCCTGATAACAGGTCCCAAGGCCTATCTGACCTACACG 220

Qy    175 ACTAGTGTTGGCCTTGGGTGTGCCCAGAGTGCACAGAGGAGTGCAAGTTCCAGTTTGCTGG 234
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ACTAGTGTGGCCTTGGGTGTGCCCAGAGTGGCATCGAGGAGTGCAAGTTCCAGTTTGCTTGG 280

Qy    235 GAACGCTGGAACTGCCCTGAAAATGCTCTTCAGCTCTCCACCCACACAGGCTGAGAAGT 294
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 GAACGCTGGAACTGCCCTGAAAATGCTCTTCAGCTCTCCACCCACACAGGCTGAGAAGT 340

Qy    295 GCTACCAGAGAGACTTCCTTCATCACGCTCTGCTGAGTCAGTGACATCATC 354
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 GCTACCAGAGAGAGACTTCCTTCATCACATGCTATCAGCTCTGCTGAGTCATCATCTACATCATC 400

Qy    355 ACCAAGAAACTGTAGCATGGGTGACTTGGCATTGAAAAACTGTGGGCTTCAAACAATGA 414
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 ACCAAGAAACTGTAGCATGGGTGACTTGGCATTGAAAAACTGTGGGCTTCAAACAATGA 460

Qy    415 AAAACAGGAGGGCCCATGGCTGGATCTGGGGAGGCTGCAGCGACAAATGTGGAATTGGGGAA 474
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 AAAACAGGAGGGCCCATGGCTGGATCTGGGGGAGGCTGCAGCGACAAATGTGGAATTTGGGGAA 520

Qy    475 AGGATCTCCAAACTCTTTGTGGACAGTTTGGGAGAGAGGGAAGGATGCCAGAGAGCCCTGATG 534
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    534 [continues]
```

```
RESULT 2
US-10-451-168-11
Sequence 11, Application US/1045168

GENERAL INFORMATION:
 APPLICANT: SMITHKLINE BEECHAM CORPORATION
 APPLICANT: SMITHKLINE BEECHAM p.l.c.
 APPLICANT: GLAXO GROUP LIMITED
 TITLE OF INVENTION: NOVEL COMPOUNDS
 FILE REFERENCE: GP50039
 CURRENT APPLICATION NUMBER: US/10/451,168
 CURRENT FILING DATE:   2003-11-12
 PRIOR APPLICATION NUMBER: PCT/US01/49232
 PRIOR FILING DATE: 2000-12-17
 PRIOR APPLICATION NUMBER: 60/256,710
 PRIOR FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: 60/257,048
 PRIOR FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: 60/260,482
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/264,922
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 60/266,797
 PRIOR FILING DATE: 2001-02-06
 PRIOR APPLICATION NUMBER: 60/276,988
 PRIOR FILING DATE: 2001-03-19
 PRIOR APPLICATION NUMBER: 60/281,535
 PRIOR FILING DATE: 2001-04-04
 PRIOR APPLICATION NUMBER: 60/289,622
 PRIOR FILING DATE: 2002-06-28
 NUMBER OF SEQ ID NOS: 110
```

```
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 11
 LENGTH: 1056
 TYPE: DNA
 ORGANISM: Homo sapiens
US-10-451-168-11

Query Match        88.9%;  Score 986.4; DB 7;  Length 1056;
Best Local Similarity  99.4%;  Pred. No. 1.8e-301;
Matches 990; Conservative  0; Mismatches  6;  Indels  0;  Gaps  0;
```

```
Db   961 ACGGTCAAGGTCTGACCAGTGTGTAGGCATGTGGTGGACCAAGTATTACTCGCGACGCTCCCCA 1020
             ||||||||||||||||||||||||||||||
Qy  1075 GGCACTGCCCAGTCCCTGGGTAAGGCAGTGCCTGA 1110
             |||||||||||||||||||||||||||||||||
Db  1021 GGCAGTGCCCAGTCCCTGGGTAAGGCAGTGCCTGA 1056
```

RESULT 3
PCT-US03-37355-53
; Sequence 53, Application PCT/US0337355
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND TISSUE
; TITLE OF INVENTION: REGENERATION
; FILE REFERENCE: HYDR-PW1-004
; CURRENT APPLICATION NUMBER: PCT/US03/37355
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 53
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-37355-53

Query Match   15.3%; Score 170; DB 1; Length 1506;
Best Local Similarity 54.2%;
Matches 413; Conservative 0; Mismatches 340; Indels 9; Gaps 3;

Qy 171 CACGACTAGTGTGTGGCCTTGGGTGTGCCCAGAGTGGCCATCGAGAGGAGGTGCAAGTTCCAGTTTGC 230
             ||| |||| ||| ||||| ||| |||| ||||| || ||||| |
Db 314 CATGCCCAGCGTGGCCCGAGGGCGTGAAGCTGGGCATCCAGGAGTGCCAGCACCAGTTCCG 373

Qy 231 TTGGGAACGCTGGAACTGCCCTGAAAAATGCTCTTCAGCTCTCCACCCACAA---CAGGCT 287
             |||||| |||| | | | | ||| || |||||| || ||| |||
Db 374 GGGGCCGCCTGGGAACTGCACCACCATAGATGACAGCGCCATCTTTGGGCCGTCTCT 433

Qy 288 GAGAGTGCTACCAGAGAGACTTCCTTCGTTCATCATGTCTATCACGCCTGCTCTGCTGGAGTCATGTA 347
             |||||| || |||||| | ||| | | || || |||||| || | ||||||| ||
Db 434 CGACAAAGCCACCACCGGAGTCGGCGCCTTCGAGTGGCGTGCCTTCGCACGGTGTTCCGCTTGGAACTG 493

Qy 348 CATCATCACCAAGAACTGTAGCATGGGTGACTTCGAAAACTGTGGCTGTGATGGGTGTCAAA 407
             |||| |||| | || || | |||| ||| | ||| |||||||| | |||||
Db 494 CGCCGTCACCCGCTCCTGCCCGAGGGCACCTCCACCATTTGCGGTGTTGCACAAGTGTGGCCGTCA 553

Qy 408 CAATGGAAAAACAGGAGGAGGCCATGGATGCGGATCTGGGGGAGGGGCTGCAGCGACAATGTGGAAATT 467
             || ||||| | |||| || ||| || || ||||| ||||| |||| | || || ||||| |
Db 554 TAAGGG---GCCGCCTGGCGAAGGCTGGAGTGGGGCGGCCGCTCCAGCGAGGCACCCAGAGGCCTGAGGT 610

Qy 468 TGGGGAAAGGATCTCCAAAACTCTTTGTGGGACAGTTTGGGAGAAGGGAAGGATGCCAGAGC 527
             ||||| | |||||| ||| ||| | || ||||| ||||| | || ||| | | |||
Db 611 CGGCGGTGTTAGTGTCCAGGGAGTTCCGGACTGCGGCCGGAACACAGCGCCGGCGGCTC 670

Qy 528 CCTGATGAATCTTCACAACACAGGGCGGCCGCAGACTGGCCAGTGAGAGCTCACCATGAAAAG 587
             |||| ||||| ||| | | ||| | | | ||| ||||||||| | | |||| |||
Db 671 GGCCCATGAACAAGCACAACGAGACTATTCCTGGACAGAGCCCACACATGCACCT 730

Qy 588 GACATGCAAAATGTCATGGGCATCTCTGGGAGTGGCATCATGACGCTGGCTGCTGCGCAGCT 647
             |||| || | ||||||||| | | ||||||| || | | || | || | |||||
Db 731 CAAATGCAAGTGCCACCGGGCTGCTGTGAGGTGAAGAACCTGCTGTCGTGGGCGCCA 790

Qy 648 GGCTGGAATTCCGGGAGGATGGGGAGACTACCTAAAGGCCAAGTAGTGATGGACCAGTGAAAAT 707
             ||||| | || ||||| ||||||| |||| ||||||| | |||||| || |||||
Db 791 GCCTGGACTTCCGGTGCCATCGCTGCCAAGGTATGACAAGTGCCACGG 850

Qy 708 TGAAATGGATAAGCGGGCAGCGACTGAGAGAGCTGGGAACAGGCCCACTGGGTGCCCGGC 767
             || | |||| | || | || || ||| || ||| || || || ||| || || ||
Db 851 GGTAGTAGAGAA---GCACCGGTGAGTCCTGAGACCCTGGGTGACCCCTGGGTCACCAAGTA 907

Qy 768 TGAGGGCCTTCCTTTCTTTTTTAGAGGAATCACCCAGATTA 827
             ||||| |||| | ||| |||||| | | | |||
Db 908 CTCGCTCTTCAAGCCACCACCGGGAGAGGAGGGGGGACCTGGTCTACTACGAGAACTCCCCAAACTT 967
```

RESULT 4
PCT-US03-04188-1
; Sequence 1, Application PCT/US0304188
; GENERAL INFORMATION:
; APPLICANT: CuraGen Corporation, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; TITLE OF INVENTION: OF USE
; FILE REFERENCE: 15966-744CIP PCT
; CURRENT APPLICATION NUMBER: PCT/US03/04188
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,375
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/387,082
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 1
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1047)
PCT-US03-04188-1

Query Match    14.8%;  Score 164.4;  DB 1;  Length 1047;
Best Local Similarity  54.0%;
Matches  402;  Conservative  0;  Mismatches 336;  Indels  6;  Gaps  3;

```
Qy  828 CTGTACCTTGCCGAATTCCAGCCTTGGGCATCTATGGCACAGGAGGGTTCGGTGAGTGCGTCTACGAGA 887
             |||  |||||| || |  ||  | ||||  | ||   || || || || |  ||||| ||||
Db 1028 CTCCCACGGGCATCGGATGGCTGCGGATCTGCTCTGCCTGTGGGCCG 1069

Qy  888 CACCCACAACACATTCCAGGTGGGAGGACCGACGTAGCCTGTTGGGACTG 929
             |||||||| || || | |||| ||||||| |  ||| ||||||||||
Db  968 TTGTGAGCCACCACCAGAGACGGGGTTCCTTTGGCACAAGGGACCGGA 929

Qy  189 GGGTGCCCAGAGTGGCCATCGAGGAGGTGCAAGTTCCAGTTTGCTTGGGAACGCTGGAACTG 248
             ||| |||  |||| | ||||  | |  ||||| | ||||   | ||||| | ||||
Db  192 GGGGGCGCGAGATGGGCCATCAACGAGTGCCAGTTCCGTTTCCGCTTGGAACTG 251

Qy  249 CCCTGAAAAATGCTCTTCAGCTCTCCACCCACAACAGGCTGAGAGTGCTACCAGAGAGAC 308
             |||| ||| | || || | | | || || |  || |  | |||| || | | ||||
Db  252 CTCTGCCCTCGCGGAGAAGACCGTCTTCGGGCCGTCTTCGGGGAACTGCGCCGTCACCCGCTC 311

Qy  309 TTCCTTCATACATGCTATCAGCTTGTTTGGAGTTGGGCTGTGATGGGTGTCAAACAATGG---AAAAACAGGAGG 368
             ||||| || | || | ||||| |  || || ||||| ||  || | |||||||  |||
Db  312 TGCCTTCACGTACCGCCATCACCCGCGTTCCGGTTCATCGTTACATCACCAAGAACTGTAG 371

Qy  369 CATGGGGTGACTTCGAAAAACTGTGGGCTGTGATGGGTGTCAAACAATGG---AAAAACAGGAGG 425
             |||||| |||  | ||||  |||||| ||| |   |||| | |  |||
Db  372 CCAAGGGAAACCTGAGACAACTGCGCCGCTCGCAGAGCAGGCGGCTACTACAACCAAGC 431

Qy  426 CCATGGCTGGATCTGGGGAGGCCGTCCAGCGACAAGTGGAATTTTGGGGAAAAGGAATCTCCAA 485
             |||| |||  |||||  | || | || | || || | | || |||| ||| |||| |||| ||
Db  432 CGAGGGCTGGAAGTGGGGCGGCCGCTCCCGGCGATCGACGTGCCGGCATCGACTTCTCCG 491

Qy  486 ACTCTTTGTGGACAGTTTGGAGAAGGGGAAGGGTGCAGAGCGCCCTGATGAATCTTCACAA 545
             ||| |||||||| | | |||| || ||| |||| | ||  |||  || ||| ||| |||||
Db  492 GCCCTTCGTTGGACAGCCTCGGGAGGATCAAGAAGAACCAGGTTCCTGGAAGTTCATGGG 551

Qy  546 CAACAGGCGGCCGCCCCAGGAACATGGCCAGTGAGCGACCACCACCATGAAAAGGACATGCATGG 605
             || | ||| | ||  || || || ||||   | | |||| |   |||||||  |||  ||
Db  552 CAATGAGCCGGCGGGAGAAGGGTTCTTAGGAGGACCCGGATCGAGCGTCCGGCAAGTGCCACGG 611

Qy  648 GCCTGACTTCCGGTGCCATCGCTGCCAAGGTATGACAAGTGCCACGG 707
             |||| || || ||||| |||  |||||  | |||| |||||||||
Db  612 CGTGTCTCGGCTCCTGCACCACCAAAACCTGCTCGGAACCTGCTGTCGTGGGCGCCA 671

Qy  606 CATCTCTGGGAGCTGCAGCATACGACATGCTGGCTGCTGCGCAGCT 665
             |||| ||| || |  || | || || || ||||  | |||||
Db  552 CAATGAGCCGGCGGGAGAAGGGTTCTTAGGAGGACCCGGATCGAGCGTCCGGCAAGTGCCACGG 611

Qy  708 TGAAATGGATAAGCGGGCAGCGACTGAGAGAGCTGGGAACAGGCCCACTGGGTGCCCGGC 767
             || | |||| | || | || || ||| || ||| ||  | | ||| || || || ||
Db  672 GGGCCACCTGCTGTGAAGGAGAAGTACTACAACGCGGCGGCGTGGCAGGAGGTGG-TGCGGGGCA 730

Qy  768 TGAGGGCCTTCCTTTCTTTTTTAGAGGAATCACCCAGATTA 827
             ||||| ||||  |   |||  |||||| |   | | |||
Db  666 GGGAGACTACCTAAAAGGCCGCTGAAAATTGAAAATGGATAAAGCGGCA 725
```

RESULT 5
US-10-364-888-1
Sequence 1, Application US/10364888

GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Zhong, Haihong
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gangolli, Esha
; APPLICANT: Guo, Xiaojia
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Shimkets, Richard
; APPLICANT: Spytek, Kimberly
; APPLICANT: Vernet, Corine
; APPLICANT: Rieger, Daniel
; APPLICANT: Edinger, Shlomit
; APPLICANT: Burgess, Catherine
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 15966-744CIP
; CURRENT APPLICATION NUMBER: US/10/364,888
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,375
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/387,082
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/625,634
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: CuraSeqlist version 0.1
;
; SEQ ID NO 1
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1047)
US-10-364-888-1

Query Match   14.8%; Score 164.4; DB 7; Length 1047;
Best Local Similarity   54.0%; Pred. No. 4.9e-41;
Matches 402; Conservative   0; Mismatches 336; Indels   6; Gaps   3;

Qy   189 GGGGTGCCCAGAGTGGGCATCGAGGAGTGCCAAGTTCCAGTTTGCTTGGGAACGTGGGAACTG 248
            |||||| |||||||||||||||||||||||||||||||||||||||||| || ||||||||
Db   192 GGGGGCGCGAGATGGGCATCAACGAGTACCAGTTCCGGCTTCGGACGGCTGGGAACTG 251

Qy   249 CCCTGAAAATGCTTCTTCACCACCAACACAGGCTGAGAAGTGCCTACCAGAGAGAC 308
            ||||||||||||| || ||||||||||||| || |||||||| |||||||||||||
Db   252 CTCTGCCTCGCGAGAGAACCGCTCTTCGGGAGTCATGTACATCATCACCAAGAACTGTTAG 311

Qy   309 TTCCTTCATACAATGCTATCAGCTTCTGCTTGGGAGTCATGTACATCACCAAGAACTGTTAG 368
            ||| ||| || ||| || | || || |||||||||||||||||||||||||||||||
Db   312 TGCCTTCACGTACGCCATCACCGGCGTCACCGCCGTCACCGCTGCCTCCAG 371

Qy   369 CATGGGTGACTTCGAAAACTGTGGGCTGTGATGGGTCAAACAATGG--AAAAACAGAGG 425
            |||||||||||||||| ||||||| |||||| ||||||||||
Db   369 CCCTGAAAATGCTTCTTCACCACCAACACAGGCTGAGAAGTGCCTACCAGAGAGAC 308

Qy   726 GCTGAGAGCTGGGAAACAGCGCCGAGGCGCCACTGGGTGCCCGTGGGTGCCCGTGAGGCCTTCCTTCCTTAG 785
            |||| |||||||||| |||||||||||||||||||||| | |||||||| ||||||||||
Db   731 GCCGCTGCGCGCGCGCCGCCGCCACCTTCCTCGCGGCCATCAAACAGCGCTGCGCGCAG--CTATCAGAAGCC 788

Qy   786 CGCAGAGACGCGGAACTGATCTTTTTAGGGAATCACCAGATTACTGTACCTGCAATTCCAG 845
            ||||||||||||| || ||||||||||| | ||||||||||| ||||||||||||||||||
Db   789 CATGGAGACAGACCTGGTGTACATTGAGAAGTCGCCCAACTACTGCCAGGAGGAGACGCGGGC 848

Qy   846 CCTGGGCATCTATGGCACAGAGGGGTTCGTGAGTGCCTACAGACAGCCACCACACATCCAG 905
            |||||| ||||| |||| |||| |||||||||||||||||| |||||||| ||||||
Db   849 CACGGGCGAGCGCGTGGGCACGCAGGGCCCGTCTCCGACACCGCAGGTCGCCCGGGACGG 908

Qy   906 GTGGGACCGACCTAGCGTGTGGGCG 929
            ||||||||||||| ||||||||||
Db   909 CTGTGACACCATGTGCTGCGGCCG 932

RESULT 6
PCT-US03-04188-7
Sequence 7, Application PC/TUS0304188

GENERAL INFORMATION:
; APPLICANT: CuraGen Corporation, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 15966-744CIP PCT
; CURRENT APPLICATION NUMBER: PCT/US03/04188
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,375
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/387,082
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: CuraSeqlist version 0.1
;
; SEQ ID NO 7
; LENGTH: 2160
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1052)
PCT-US03-04188-7

Query Match   14.8%; Score 164.4; DB 1; Length 2160;
Best Local Similarity   54.0%; Pred. No. 6.8e-41;
Matches 402; Conservative   0; Mismatches 336; Indels   6; Gaps   3;

Qy   189 GGGGTGCCCAGAGTGGGCATCGAGGAGTGCCAAGTTCCAGTTTGCTTGGGAACGTGGGAACTG 248
            |||||| |||||||||||||||||||||||||||||||||||||||||| || ||||||||
Db   197 GGGGGCGCGAGATGGGCATCAACGAGTACCAGTTCCGGCTTCGGACGGCTGGGAACTG 256

Qy   249 CCCTGAAAATGCTTCTTCACCACCAACACAGGCTGAGAAGTGCCTACCAGAGAGAC 308
            ||||||||||||| || ||||||||||||| || |||||||| |||||||||||||
Db   249 CCCTGAAAATGCTTCTTCACCACCAACACAGGCTGAGAAGTGCCTACCAGAGAGAC 308

Qy   372 CCAAGGGGAACCTGAGCAACTGCGCGCTGCGACCCGCGAGAAGCAGGCGTACTAACCAAGC 431
            |||| || ||| | || || | || | ||||| ||||||||||
Db   372 CCAAGGGGAACCTGAGCAACTGCGCGCTGCGACCCGCGAGAAGCAGGCGTACTAACCAAGC 431

Qy   432 CGAGGGCTGGAAGTGGGGCGGCGGCTTGCTCGGGCCGACGTGCGTTACGGCATCGACTTCTCCG 491
            |||||||||||||||| || |||| | ||||||||| ||||||| ||||||
Db   426 CCATGGGCTGGGATCTGGGGAGGGCCTGGCAGGGCACAATGTGAATTGGGGAAAGGATCTCCAA 485

Qy   546 CAACAGGAGGCCCGGCAGACTGGGCAGTGAGAGCCACCATGAAAAAGACATGCAAAAATGTCATGG 605
            |||||||||| ||||||| || ||||||| || |||||||||||| |||||||| |||||||
Db   492 GCCGCTTCGTGGACGCTCGGGAGGATCAAGAGAACGGCGGCCTCATGAACCTGCATAA 551

Qy   606 CATCTCTGGGAGCTGCAGCATACAGACAGAATGCTGGCTGCGAGCTGGCTGAATTCGGGAGGT 665
            ||||||||||||||| |||| ||||| | ||| || || || || |||||||||||||||
Db   552 CAATGAGGCGCGGCAGGAGAAGGTTCTAGAGACGACCGGATGCAGCTGGCTGGAGTCCACGG 611

Qy   666 GGGAGGACTACCTAAAAGGCCAAGTAATGACCAGGGGCTGAAAATTGAAATGGATAAAGCGGCA 725
            |||||||| || ||||| |||||| || || |||||||||| ||| ||||| |||||||| |
Db   612 CGTGTGTCTCGGCTTGCGCTCCTTGCCACCACAAAAACCTGCTTCGGACCACACAGCTGCAGCTGGC 671

Qy   726 GCTGAGAGCTGGGAAACAGCGCCGAGGCGCCACTGGGTGCCCGTGGGTGCCCGTGAGGCCTTCCTTCCTTAG 785
            ||||| |||||||||| |||||||||||||||||||||| | |||||||| ||||||||||
Db   672 GGGCCCACCTGCTCGAAGGAGAGAGTACAAACGGCGGCCGTGCAAGGTGGG-TCGGGGCCA 730

Qy   786 CGCAGAGACGCGGAACTGATCTTTTTAGGGAATCACCAGATTACTGTACCTGCAATTCCAG 845
            ||||||||||||| || ||||||||||| | ||||||||||| ||||||||||||||||||
Db   731 GCCGTCTCGCCGCAGCCCACCTTCCTCGCCATCAAAACACTGCCCGCAG--CTATCAGAAGCC 788

Qy   846 CCTGGGCATCTATGGCACAGAGGGGTTCGTGAGTGCCTACAGACAGCCACCACACATCCAG 905
            |||||| ||||| |||| |||| |||||||||||||||||| |||||||| ||||||
Db   849 CACGGGCGAGCGCGTGGGCACGCAGGGCCCGTCTCCGACACCGCAGGTCGCCCGGGACGG 908

Qy   906 GTGGGACCGACCTAGCGTGTGGGCG 929
            ||||||||||||| ||||||||||
Db   909 CTGTGACACCATGTGCTGCGGCCG 932

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 13:22:49 ; Search time 44 Seconds
                 (without alignments)
                 1331.139 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCCIQCCLVSPFTLTFC..........SKYYCARSPGSAQSLGKSSA 369

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1808	88.8	351	23	AAM47902	Human wingless-lik
2	1804	88.6	351	23	ABP60975	Novel human protei
3	1802	88.5	351	23	AAM47662	Novel human protei
4	1783	87.5	415	22	AAE02906	MOL4 protein seque
5	1779	87.3	415	24	ABG72362	Human Wnt3 (ZWnt3)
6	1496	73.4	354	22	AAE02907	Human wingnut prot
7	1213	59.5	351	22	ABG12429	Murine Wnt-8D prot
8	1213	59.5	351	24	AAE34045	Novel human diagno
9	1213	59.5	351	24	ABU55891	Human WNT-8B prot
10	1137.5	55.8	295	22	AAB02909	Human Wnt-8B prote
11	654.5	32.1	380	23	AAU85413	Human protein NOV1
12	649.5	31.9	359	21	AAY57271	Wnt-4AF and Wnt-5c
13	649.5	31.9	359	23	ABG61843	Prostate cancer-as
14	649.5	31.9	372	24	AAE34040	WNT-2B protein. U
15	649.5	31.9	372	24	ABU55884	Human WNT-2B prot
16	649.5	31.9	372	24	ABU07452	Protein different1
17	648	31.8	351	20	AAY41719	Human PRO864 prote
18	648	31.8	351	21	AAB44275	Human PRO864 (UNQ4
19	648	31.8	351	21	AAY57270	Wnt-4AF and Wnt-5c
20	648	31.8	351	24	ABU55608	Human secret/tra
21	648	31.8	351	22	AAU29063	Human PRO polypept
22	648	31.8	351	22	AAM38889	Human polypeptide
23	648	31.8	351	21	ABU71151	Human PRO864 proce
24	648	31.8	351	24	ABU65608	Human secret/tra
25	648	31.8	351	24	ABU65941	Novel human secret
26	648	31.8	351	24	ABU67445	Human PRO polyp
27	648	31.8	351	24	ABU61105	Human PRO polyp
28	648	31.8	351	24	ABU65303	Human PRO polypept
29	648	31.8	351	24	ABU58439	Human PRO polypept
30	648	31.8	351	24	ABU55975	Human secreted/tra
31	648	31.8	351	24	ABU56970	Human PRO polypept
32	648	31.8	351	24	ABU10549	Human secreted/tra
33	648	31.8	351	22	AAE09707	Human polypeptide
34	648	31.8	365	22	AAM40675	Human gene 3 encod
35	640.5	31.4	360	21	AAY70734	Human Wnt-2 protei
36	640.5	31.4	360	24	AAE34039	Human Wnt-2 protei
37	640.5	31.4	360	24	AAY57595	WNT-2 protein. Un
38	640.5	31.4	360	24	ABU55883	Human WNT-2 prote
39	637	31.3	370	21	AAB19786	Human Wnt-1 protei
40	636.5	31.2	365	21	AAY70739	Human Wnt-5a prote
41	636.5	31.2	365	21	AAY57600	Human Wnt-5a prote
42	636.5	31.2	365	22	AAB73619	Wnt-5a tumour supp
43	636.5	31.2	365	23	AAU85414	Human protein NOV1
44	636.5	31.2	365	24	AAE34041	WNT-4 protein. Un
45	636.5	31.2	365	24	ABP58342	Human cell growth,

ALIGNMENTS

RESULT 1
AAM47902

ID   AAM47902 standard; Protein; 351 AA.
XX
AC   AAM47902;
XX
DT   25-FEB-2002   (first entry)
XX
DE   Human wingless-like Wnt-8D SEQ ID NO 2.
XX
KW   Human; wingless-like gene; Wnt-8D; antiasthmatic; nootropic; vaccine;
KW   neuroprotective; cytostatic; antidepressant; neuroleptic; vasotropic;
KW   cerebroprotective; vulnerary; asthma; Alzheimer's disease; cancer;
KW   cardiomyopathy; depression; schizophrenia; ischaemia; stroke;
KW   wound healing; kidney disease; lung disorder; apoptosis;
KW   stem cell therapy; immunological response; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200183543-A1.
XX
PD   08-NOV-2001.
XX
PF   30-APR-2001; 2001WO-EP04887.
XX
PR   03-MAY-2000; 2000EP-0109422.
XX
PA   (MERE) MERCK PATENT GMBH.
XX
PI   Duecker K;
XX
DR   WPI; 2002-034504/04.

```
DR   N-PSDB; ABA05327.
XX
PT   New wingless/int 8D polypeptide, useful for treating asthma,
PT   Alzheimer's disease, cancer, ischaemia, stroke, depression,
PT   schizophrenia, aberrant apoptosis and for identifying modulators of
PT   polypeptide activity -
XX
PS   Claim 4; Page 37-38; 43pp; English.
XX
CC   The invention relates to a polypeptide (I) having a fully defined
CC   wingless/int 8D (Wnt-8D) protein sequence of 351 amino acids (AAM47902)
CC   or is encoded by a defined polynucleotide sequence (II) of 1650
CC   nucleotides (ABA05327) or is a polypeptide having 95% identity to (I) or
CC   fragments or variants of above mentioned polypeptides. (I) has
CC   antiasthmatic, nootropic, neuroprotective, cytostatic, antidepressant,
CC   neuroleptic, vasotropic, cerebroprotective and vulnerary activity. (I) is
CC   useful for identifying compounds that stimulate or inhibit the function
CC   or level of the polypeptide. (I) and (II) are useful for treating asthma,
CC   Alzheimer's disease, cancer, cardiomyopathies, depression, schizophrenia,
CC   general psychotic disorders, ischaemia, stroke, wound healing, kidney
CC   diseases, lung disorders, aberrant apoptosis, tissue remodeling, stem
CC   cell therapies. (I) and (II) are also useful as vaccines for inducing an
CC   immunological response in a mammal and in gene therapy.
XX
SQ   Sequence   351 AA;

Query Match             88.8%;  Score 1808;  DB 23;  Length 351;
Best Local Similarity   98.2%;
  Matches  331;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy     33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy     93 HNRLRSATRETSFIHAISSAGVWNYIIITRNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     75 HNRLRSATRETSFIHAISSAGVWNYIIITRNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 134

Qy    153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGIGSGSCSIQTC 212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGIGSGSCSIQTC 194

Qy    213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWWPAEAFLPSAEAELIFLEE 272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy    273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy    333 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 369
          |||||||||||||||||||||||||||||||||||||
Db    315 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 351
```

```
RESULT 2
ABP60975
ID   ABP60975 standard; Protein; 351 AA.
XX
AC   ABP60975;
XX
DT   10-SEP-2002 (first entry)
XX
DE   Novel human protein. SEQ ID 62.
XX
KW   Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
KW   nootropic; neuroprotective; immunosuppressive; haemostatic;
KW   antiinflammatory; cardiant; antiulcer; viruicide; antithyroid;
KW   cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW   wound healing disorders; atherosclerosis; Parkinson's disease;
KW   Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW   inflammation; neoplastic disease; nervous system disorder;
KW   cardiovascular disorders; pancreatitis; respiratory disorder;
```

```
KW   hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW   developmental abnormality; gastrointestinal ulceration; neuropathy;
KW   haematological disease; metabolic disease; sperm dysfunction;
KW   thyroid disorder; hypothyroidism; brain damage; colitis;
KW   cone photo- transduction deficiency; neurological disease; stroke;
KW   angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW   trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW   growth abnormality; precocious puberty.
XX
OS   Homo sapiens.
XX
PN   WO2002050105-A1.
XX
PD   27-JUN-2002.
XX
PF   17-DEC-2001; 2001WO-US49232.
XX
PR   19-DEC-2000; 2000US-256710P.
PR   20-DEC-2000; 2000US-257048P.
PR   09-JAN-2001; 2001US-260482P.
PR   09-JAN-2001; 2001US-260482P.
PR   30-JAN-2001; 2001US-264922P.
PR   06-FEB-2001; 2001US-267797P.
PR   19-MAR-2001; 2001US-276988P.
PR   04-APR-2001; 2001US-281535P.
PR   08-MAY-2001; 2001US-289622P.
XX
PI   Agarwal P, Birkeland M, Cogswell JP, Kabnick KF, Lai Y;
PI   Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
XX
DR   WPI; 2002-508784/54.
DR   N-PSDB; ABQ86140.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PT   Secreted proteins and polynucleotides useful as vaccines for preventing
PT   or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT   Parkinson's disease, Alzheimer's disease, infection, autoimmune
PT   disorder -
XX
PS   Claim 1(a); Page 267-268; 335pp; English.
XX
CC   The invention relates to an isolated polypeptide with signal sequences
CC   which allow it to be secreted extracellularly or membrane associated.
CC   The activity of polypeptides of the invention may be described as,
CC   cytostatic, vulnerary, antiarteriosclerotic, antiinflammatory, nootropic,
CC   neuroprotective, immunosuppressive, haemostatic, antiparkinsonian,
CC   cardiant, antiulcer, viruicide, antithyroid, cerebroprotective, anorectic,
CC   and metabolic. Polypeptides and polynucleotides of the invention are
CC   useful in the treatment, or as a vaccine in the prevention of, cancer,
CC   wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC   and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC   inflammation, neoplastic diseases, nervous system related disorders and
CC   cardiovascular disorders, pancreatitis, respiratory disorder,
CC   hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC   developmental abnormality, gastrointestinal ulceration, neuropathy,
CC   haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC   disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC   transduction deficiency, neurological diseases, stroke, angiogenesis,
CC   ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC   trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC   growth abnormalities, and alleviation of precocious puberty. The
CC   sequences given in records ABP60965-ABP61019 represent novel human
CC   proteins of the invention.
XX
SQ   Sequence   351 AA;

Query Match             88.6%;  Score 1804;  DB 23;  Length 351;
Best Local Similarity   97.9%;
  Matches  330;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
```

```
Db   15 CAAFSASAWSVVNNFLITGPKAYLTYTTSVALGAQSGIEBCKFQFAWERWNCPENALQLST 74
            ||  |   ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNGSMGDFENCGGCDGSNNGKTGGHGWIWGGCSD 152
Db   75 HNRLRSATRETSFIHAISSAGVMYIITKNGSMGDFENCGGCDGSNNGKTGGHGWIWGGCSD 134
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
Db  135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLVVRATMKRTCKCHGISGSCSIQTC 194
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
Db  195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
Db  255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  333 KFPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 369
Db  315 KFPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 351
```

RESULT 3
AAM47662

ID   AAM47662 standard; Protein; 351 AA.
XX
AC   AAM47662;
XX
DT   21-FEB-2002 (first entry)
XX
DE   MOL4 protein sequence.
XX
XX
XX
OS   Unidentified.
XX
WO200181578-A2.
XX
01-NOV-2001.
XX
26-APR-2001; 2001WO-US15578.
XX
30-JAN-2001; 2001US-265160P.
22-JAN-2001; 2001US-263217P.
15-SEP-2000; 200US-232678P.
25-JUL-2000; 2000US-220591P.
03-MAY-2000; 2000US-201508P.
03-MAY-2000; 2000US-201474P.
03-MAY-2000; 2000US-201486P.
02-MAY-2000; 2000US-201238P.
01-MAY-2000; 2000US-201236P.
01-MAY-2000; 2000US-201007P.
01-MAY-2000; 2000US-201006P.
28-APR-2000; 2000US-200780P.
28-APR-2000; 2000US-200613P.
26-APR-2000; 2000US-200158P.
XX
(CURA-) CURAGEN CORP.
XX
Vernet CAM, Fernandes ER, Gerlach V, Shimkets RA, Malyankar UM;
Boldog FL, Zerhusen BD, Spytek KA, Majumder K, Tcherniev VT;
Padigaru M, Patturajan M, Burgess CE, Gangolli EA, Smithson G;
Rastelli L, Macdougall JR, Taupier RJ, Grosse WM, Szekeres ES;
Alsobrook JP;
XX
XX

DR   WPI; 2002-049278/06.
DR   N-PSDB; ABA04592.
XX
XX
PT   Novel G-protein coupled receptor-related polypeptides and
PT   polynucleotides for diagnosing, preventing and treating cardiomyopathy,
PT   atherosclerosis, disorders related to cell signal processing and for
PT   identifying modulators
XX
PS   Claim 1; Page 34; 227pp; English.
XX
CC   The present invention relates to novel G-coupled protein-receptor related
CC   proteins and coding sequences (MOLX, where X is a number from 1 to 10,
CC   ABA04589-ABA04603 and AAM47659-AAM47673). MOLX proteins and coding
CC   sequences are useful for treating or preventing a MOLX-associated
CC   disorder, such as cardiomyopathy, atherosclerosis, disorders related to
CC   cell signal processing and metabolic pathway modulation, diabetes and
CC   cancer. Additionally, MOLX proteins and coding sequences are useful for
CC   preventing and treating a variety of disorders including metabolic
CC   disorders, nutritional oedema, chronic and hereditary pancreatitis,
CC   obesity, infectious disease, anorexia, neurodegenerative disorders,
CC   Alzheimer's disease, Parkinson's disease, stroke, immune disorders,
CC   and wasting disorders associated with chronic diseases and cancers,
CC   haematopoietic disorders and various dyslipidaemias, metabolic syndrome X
CC   cardiac disorders, hypertension, hypercalcaemia, cirrhosis, angiogenesis
CC   and wound healing, trauma, glomerulonephritis, hyper and hypothyroidism,
CC   multiple sclerosis, lung diseases including asthma, Crohn's disease,
CC   scleroderma, autoimmune diseases, developmental disorders and neural tube
CC   defects. The present sequence is the protein sequence for MOL4.
CC   MOL4 is a Wnt 8-like protein.
XX
XX
SQ   Sequence 351 AA;

Query Match   88.5%; Score 1802; DB 23; Length 351;
Best Local Similarity   97.9%; Pred. No. 2.3e-162;
Matches 330; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEBCKFQFAWERWNCPENALQLST 92
            |||   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15 CAAFSASAWSVVNNFLITGPKAYLTYTTSVALGAQSGIEBCKFQFAWERWNCPENALQLST 74
Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNGSMGDFENCGGCDGSNNGKIGHGHGWIWGGCSD 152
           |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||
Db   75 HNRLRSATRETSFIHAISSAGVMYIITKNGSMGDFENCGGCDGSNNGKTGGHGWIWGGCSD 134
Qy  153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLVVRATMKRTCKCHGISGSCSIQTC 194
Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254
Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314
Qy  333 KFPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 369
           ||||||||||||||||||||||||||||||||||||||
Db  315 KFPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 351
```

RESULT 4
AAE02906

ID   AAE02906 standard; Protein; 415 AA.
XX
AC   AAE02906;
XX
DT   10-AUG-2001 (first entry)
XX
DE   Human Wnt3 (ZWnt3) protein.
XX
KW   Human; ZWnt3; gene therapy; cellular signalling; education tool;
KW   tissue development; biopharmaceutical; antibody production; glycoprotein.

```
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 171
FT                  /note= "Encoded by GTG"
XX
PN   WO200138353-A2.
XX
PD   31-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US31820.
XX
PR   22-NOV-1999; 99US-0444788.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Holloway JL;
XX
DR   WPI; 2001-367660/38.
DR   N-PSDB; AAD06571.
XX
PT   Zwnt3 polypeptides useful for producing antibodies, for
PT   biopharmaceuticals, and as educational tools in laboratory practical
PT   kits -
XX
PS   Claim 1; Page 3; 82pp; English.
XX
CC   The present sequence is human Wnt3 (Zwnt3) protein which is a
CC   cellular signalling molecule. Wnt proteins are a family of secreted
CC   glycoproteins, which, in many organisms, have a role in morphological
CC   development of tissues in both embryonic and adult contexts. Wnt3 DNA
CC   and protein are useful as education tools in laboratory practical kits
CC   for genetics and molecular biology, protein chemistry and antibody
CC   production, and analysis. Wnt3 protein is useful as an aid to teach
CC   preparation of antibodies, identify proteins by Western blotting,
CC   protein purification, determining the weight of expressed Zwnt3
CC   polypeptides as a ratio of total protein expressed, identifying peptide
CC   cleavage sites, coupling amino acids and carboxyl terminal tags, amino
CC   acid sequence analysis and monitoring biological activities of both
CC   native and tagged protein in vitro and in vivo. Ab is useful for
CC   purifying Zwnt3, and cloning and sequencing the polynucleotides that
CC   encodes an antibody, hence in the design of humanised antibodies.
CC   Wnt3 DNA is also useful in gene therapy.
XX
SQ   Sequence   415 AA;

Query Match             87.5%;  Score 1783;  DB 22;  Length 415;
Best Local Similarity   98.2%;  Pred. No. 1.8e-160;
Matches  326;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy   33  CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQOSGIEECKFQFAWERWNCPENALQLST  92
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15  CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQOSGIEECKFQFAWERWNCPENALQLST  74

Qy   93  HNRLRSATRETSFIHAISSAGVMYIITKNCSMGFENCGCDSSNNGKTGGHGWIWGGCSD  152
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75  HNRLRSATRETSFIHAISSAGVMYIITKNCSMGFENCGCDSSNNGKTGGHGWIWGGCSD  134

Qy  153  NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC  212
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  135  NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC  194

Qy  213  WLQLAEFREMGDYLKAXYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE  272
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  195  WLQLAEFREMGDYLKAXYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE  254

Qy  273  SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC  332
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  255  SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC  314

Qy  333  KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSL  364
         ||||||||||||||||||||||||||||||||
Db  315  KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSL  346


RESULT 5
ABG72362
ID   ABG72362 standard; Protein; 415 AA.
XX
AC   ABG72362;
XX
DT   07-FEB-2003  (first entry)
XX
DE   Human wingnut protein Zwnt3.
XX
KW   Human; wingnut; Zwnt3; signalling molecule; secreted glycoprotein;
KW   extracellular matrix; tumour; brain development.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Peptide        30..42
FT                  /note= "This peptide is claimed in claim 5"
FT   Peptide        44..62
FT                  /note= "This peptide is claimed in claim 5"
FT   Peptide        69..97
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        101..111
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        120..138
FT                  /note= "This peptide is claimed in claim 5"
FT   Peptide        143..177
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        184..215
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        217..231
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        217..248
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        231..248
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        276..297
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        321..345
FT                  /note= "This peptide is claimed in claim 4"
FT   Peptide        345..415
FT                  /note= "This peptide is claimed in claim 4"
XX
PN   US2002123103-A1.
XX
PD   05-SEP-2002.
XX
PF   03-DEC-2001; 2001US-0005947.
XX
PR   22-NOV-1999;  99US-166827P.
PR   17-NOV-2000; 2000US-0715993.
XX
PA   (HOLL/) HOLLOWAY J L.
XX
PI   Holloway JL;
XX
DR   WPI; 2003-066796/06.
DR   N-PSDB; ABS57866.
XX
PS   Claim 3; Page 2; 37pp; English.
XX
PT   Novel human Zwnt3 polypeptide useful as aid for identifying proteins by
PT   Western blotting, to teach analytical skills such as mass spectrometry
PT   and circular dichroism, and for identifying peptide cleavage sites -
XX
CC   The invention relates to an isolated human Zwnt3 polypeptide (a wingnut
CC   protein which is a signalling molecule/secreted glycoprotein, found
CC   in the extracellular matrix) that is at least 80% identical to
CC   the protein appearing as ABG72362 sequence (SI) of 415 amino acids,
CC   where the polypeptide specifically binds with an anti-Zwnt3
```

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 13:27:05 ; Search time 20 Seconds
(without alignments)
1774.312 Million cell updates/sec

Title: US-09-898-456-7
Perfect Score: 2037
Sequence: 1 MLCCIQCLCLVSPFPLTPC..........SKYYCARSPGSAQSLGKGSA 369

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_76:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1388	68.1	387	2	S18771	developmental regu
2	1379	67.7	357	2	I50690	developmental regu
3	1287.5	63.2	361	2	I50505	Wnt-8C - chicken
4	1215.5	59.7	358	2	I50506	gene wnt8 protein
5	1155	56.7	428	2	I51680	gene wnt8b protein
6	672.5	33.0	360	2	S34173	Xwnt-8b - African
7	659	32.4	352	2	A49146	wnt-5c protein - A
8	656.5	32.2	359	2	A56549	developmental regu
9	656	32.2	357	2	B56549	cell-cell signalin
10	652.5	32.0	357	2	S15013	cell-cell signalin
11	649.5	31.9	372	2	T09612	wnt-1 protein - ze
12	644	31.6	351	2	C36470	secreted glycoprot
13	643.5	31.6	360	2	B36470	Wnt-4 protein - mo
14	640.5	31.4	360	2	S00834	Wnt-2 protein - mo
15	639	31.4	369	2	S13721	int-1-like protein
16	638.5	31.3	372	2	E36470	Wnt-1 protein prec
17	636.5	31.2	365	2	A48914	Wnt-5b protein - m
18	636	31.2	370	1	TVHUT1	proto-oncogene Wnt
19	636	31.2	370	1	TVWST1	transforming prote
20	636	31.2	370	1	TVWVT1	transforming prote
21	635	30.9	352	2	A4882B	wingless homolog X
22	629	30.9	351	2	JC2451	Cwnt-4 protein pre
23	629	30.9	352	2	A39532	Wnt-3A protein - m
24	626	30.7	355	2	A35503	Wnt-3 protein - mo
25	626	30.7	379	2	D36470	Wnt-5a protein - m
26	623	30.6	349	2	H36470	Wnt-7b protein - m
27	619.5	30.4	371	1	TVXLT1	Wnt-2 protein - fr
28	606.5	29.8	352	2	S24559	transforming prote
29	602.5	29.6	360	2	T26037	hypothetical prote
30	596.5	29.3	349	2	G36470	Wnt-7a protein - m
31	593	29.1	468	2	A29650	wingless (wg) prot
32	589.5	28.9	360	2	S32695	Wnt-2 protein - Ca
33	589	28.9	365	2	JC7694	soluble-type glyco
34	586	28.8	364	2	F36470	Wnt-6 protein - mo
35	575	28.2	372	2	T10502	Wnt-7a protein - I
36	575	28.2	348	2	S32694	Wnt-1 protein - Ca
37	572.5	28.1	469	1	TVFFT1	transforming prote
38	570	28.0	398	2	T26284	hypothetical prote
39	566	27.8	333	2	JC7693	gene WNT3 protein
40	557	27.3	417	2	A47536	soluble-type glyco
41	552	27.1	417	2	B59392	Wnt10a protein pro
42	551.5	27.1	354	2	JC4152	Wnt-11 protein pre
43	551	27.0	442	2	I50110	Wnt10a protein - z
44	544.5	26.7	354	2	S34378	wnt-11 protein - m
45	532.5	26.1	353	2	151572	maternal protein -

ALIGNMENTS

RESULT 1
S18771 developmental regulator Xwnt-8 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Nov-1993 #sequence_revision 27-Oct-1995 #text_change 24-Nov-1999
C;Accession: S18771; D49764
R;Christian, J.L.; McMahon, J.A.; McMahon, A.P.; Moon, R.T.
Development 111, 1045-1055, 1991
A;Title: Xwnt-8, a Xenopus Wnt-1/int-1-related gene responsive to mesoderm-inducing grow
A;Reference number: S18771; MUID:91347916; PMID:1879349
A;Accession: S18771
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-387 <CHR>
A;Cross-references: EMBL:X57234
R;Christian, J.L.; Gavin, B.J.; McMahon, A.P.; Moon, R.T.
Dev. Biol. 143, 230-234, 1991
A;Title: Isolation of cDNAs partially encoding four Xenopus Wnt-1/int-1-related proteins
A;Reference number: A49764; MUID:91122437; PMID:1991549
A;Accession: A49764
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'QE',181-242,'T',244-291,'R',293-321 <CH2>
A;Cross-references: GB:M55058
C;Superfamily: int-1 transforming protein

Query Match   68.1%; Score 1388; DB 2; Length 387;
Best Local Similarity   75.3%;
Matches 244; Conservative 40; Mismatches 40; Indels 0; Gaps 0;

```
Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSIEEBCKFQFAWERWNCPENALQLST 92
           |||||||||||:| ||||||||||| |: | ||||:: |||| :||||||||||:  ||| :|
Db   16 CPFFTASAWSVNNFLMTGPKAYLTYSASVAVGAQNGIEECKYQFAWERWNCPESTLQLAT 75

Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
           || |||||||||:|||||||||||  || |||||||:|||||:| || :|| :||:||||||
Db   76 HNGLRSATRETSFVHAISSAGVMYTLTRNCSMGDFDNCGCDDSRNGRIGGRGWVWGGCSD 135

Qy  153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
           | |||||||||||:| | | ||||||||||||:||||| :|||||||||||||||||:|||
Db  136 NAEFGERISKLFVDGLETGQDARALMNLHNNEAGRLAVKETMKRTCKCHGISGSCSTQTC 195

Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAPLPSAEAELFLEE 272
           |||||||| : | :||| ||||| |||||| : |||:|  | |:|| |  | :| :|:|
Db  196 WLQLAEFRDIGHNLKIKHDQALKLEMDKRKMRSGNSADNRGAIADAPSSVAGSELIFLED 255

Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVBEERKTEVISSCNC 332
           ||||| |:||:| ||||||||||: ::| | ||||| :||:| ||:| :|||||::||||
Db  256 SPDYCLKNISLGLQGTEGRECLQSGKNLSQWERRSCKRLCTDCGLRVEEKKTEIISSCNC 315

Qy  333 KFPQWCCTVKCDQCRHVVSKYYCAR 356
           ||| || |: || : :||:| ||
Db
```

Db   316 KFHWCCTVKCEQCKQVVIKHFCAR 339

RESULT 2
I50690
Wnt-8C - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
R;Hume, C.R.; Dodd, J.;
Development 119, 1147-1160, 1993
A;Title: Cwnt-8C: a novel Wnt gene with a potential role in primitive streak formation a
A;Reference number: I50690; MUID:94139958; PMID:7916678
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: I50690
A;Molecule type: mRNA
A;Residues: 1-357 <HUM>
A;Cross-references: EMBL:U02097; NID:g403577; PIDN:AAA18933.1; PID:g403578
C;Genetics:
A;Gene: cwnt-8C
C;Superfamily: int-1 transforming protein

Query Match   67.7%; Score 1379; DB 2; Length 357;
Best Local Similarity   76.5%; Pred: No. 1e-106;
Matches   241; Conservative   37; Mismatches   37; Indels   0; Gaps   0;

Qy   42 SVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWRNCPENALQLSTHNRLRSATR 101
         |||||| ||||||||| :|| ||||||||:||||||| | |||||||||:||||||||||||
Db   25 SVNNFLMTGPRAYLTYSSSVVAAGAQSGMEECKFQFQFGWERWRNCPESALQLSTHNRLRSATR 84

Qy 102 ETSFIHAISSAGVMYIITKNCSMGDFENCGCGDGSNNGKTGGHGWIWGGCSDNVEFGERIS 161
         ||||:||||||||| :||:|||:|||||:|||||| | |: :|| ||||||||||||||||
Db   85 ETSFVHAISSAGVMYTLTRNCSLGDFESCGCGDDSRNGRVGGRGWVWGGCSDNVEFGERIS 144

Qy 162 KLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE   221
         |||||:|| | :||| :|||||| :|||||||||:|||||:|||||||||||||||::||
Db 145 KLFVDALETGHDTRALINLHNNEVGRLAVRATMKRACKCHGVSGSCSIQTCWLQLADFRE   204

Qy 222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNS   281
         :|:|||:|||||:|:||||| :||||||:   :|| |: ||: ||:|||:|:||||||::
Db 205 IGNYLKMKYDQAHKLEMDKRRMRAGNSADSRGATAETFHHVHSTELVFLEDSPDYCTRNA   264

Qy 282 SLGIGYGTEGRECLQNSHNTSRWERRSSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVK 341
         ||| ||||| ||| : :|:|.|||||| |||:|||| ||| |.|||:||||||| |||| |:
Db 265 SLGHHGTEGRBCLQTGKNLSQWERRSCRRLSTECGLKVEBRRTEVVSSCNCKFHWCCTVR 324

Qy 342 CDQCRHVVSKYYCAR 356
         | ||| ||:::|||
Db 325 CEQCRQLVACHFCAR 339

RESULT 3
I50505
gene wnt8 protein - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999
R;Kelly, G.M.; Greenstein, P.; Erezyilmaz, D.F.; Moon, R.T.
Development 121, 1787-1799, 1995
A;Title: Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct de
A;Reference number: I50505; MUID:95324404; PMID:7600994
A;Accession: I50505
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-361 <KEL>
A;Cross-references: EMBL:U10869; NID:g968914; PID:g968915
C;Genetics:
A;Gene: wnt8
C;Superfamily: int-1 transforming protein

Query Match   63.2%; Score 1287.5; DB 2; Length 361;
Best Local Similarity   67.3%; Pred: No. 4e-99;
Matches   230; Conservative   45; Mismatches   64; Indels   3; Gaps   2;

Qy   40 GRSVANNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWDRWKCPERALQLSTHSGLRSA   99
Db   23 GWSVANNFLMTGPKAYLVLIYSSSVAAGAQSGIEECKYQFAWDRWKCPERALQLSTHSGLRSA 82

Qy 100 TRETSFIHAISSAGVMYIITKNCSMGDFENCGCGDGSNNGKTGGHGWIWGGCSDNVEFGER 159
Db   83 NRETAFFHAISSAGVMYTLTRNCSLGDFDNCGCDDTRNGQRGGQGWLWGGCSDNVGFGEV 142

Qy 160 ISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEF 219
Db 143 ISKQFVDALETGQDARAAMNLHNNEVGRKAVKGTMQRTCKCHGVSGSCSIQTCWLQLPEF 202

Qy 220 REMGDYLKAKYDQALKIEMDKRQLR-AGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCT 278
Db 203 REVGNYLKEKYHRAVKVDL----LRGAGNSAASRGAIAETFNSISRKELVHLEDSPDYCL 258

Qy 279 CNSSLGIGYGTEGRECLQNSHNTSRWERRSSCGRLCTECGLQVEERKTEVISSCNCKFQWCC 338
Db 259 ENRTLGLPGTEGRECLRKGKNLSKWEKRTCKRLCGDCGLAVEERRAETVSSCNCKFHWCC 318

Qy 339 TVKCDQCRHVVSKYYCAR 356
Db 319 AVKCEQCRKTVTKYYCVK 336

RESULT 4
I50506
gene wnt8b protein - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999
R;Kelly, G.M.; Greenstein, P.; Erezyilmaz, D.F.; Moon, R.T.
Development 121, 1787-1799, 1995
A;Title: Zebrafish wnt8 and wnt8b share a common activity but are involved in distinct de
A;Reference number: I50505; MUID:95324404; PMID:7600994
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Accession: I50506
A;Cross-references: EMBL:U10870; NID:g968916; PID:g968917
C;Genetics:
A;Gene: wnt8b
C;Superfamily: int-1 transforming protein

Query Match   59.7%; Score 1215.5; DB 2; Length 358;
Best Local Similarity   67.3%; Pred: No. 3.7e-93;
Matches   214; Conservative   42; Mismatches   57; Indels   5; Gaps   2;

Qy   17 LTPCQGGPHCLIPIHLCLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQF   76
Db   1 MNPCQIFASLVMSI-CCHILSSTAWSVNNFLMTGPRAYLAVTSSVQAGAQSGIEBCKHQF   59

Qy   77 AWERWRNCPENALQLSTHNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCGDG 134
Db   60 AWDRWNCPESALQLSTHKGIRSATRETAFVHAISAAGVMYLTKNCSMGDFENCGCGCCDD 119

Qy 135 SNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATM 194
Db 120 SKIGRKGGRGWWGGCGSDNVNFGDRIAKLFVDALENGHDSRAAVNLHNNEAGRLAVKATL 179

Qy 195 KRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWV 254
Db 180 KRTCKCHGLSGSCSIQTCWMQLADFRDIGSYLKIKHDQARKLEMDKIRMRAGNSADNRGA 239

Qy 255 PAEAFLPSAEAELIFLEESPDYCTCNSSLGIGYGTEGRECLQNSHNTSRWERRSSCGRLCTE 314
Db 240 IADTFSAVAGTELIFMEDSPDYCVRNLSMGLHGTEGRECLQSSGKNLSQWERRSRRLCTN 299

Qy 315 CGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCAR 356
Db 300 ACLKVEBRIETVSSCNCKFHWCCTVKCETCTQTVTRYFCAK 341

OM protein - protein search, using sw model
Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

Run on: January 30, 2004, 13:23:24 ; Search time 17 seconds
                 (without alignments)
                 1020.756 Million cell updates/sec

Title: US-09-898-456-7
Perfect Score: 2037
Sequence: 1 MLCCIQCLCLVSPFPLTPC.............SKYYCARSPGSAQSLGKGSA 369

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	Match DB	ID	Description
1	1791	87.9	355	1	WN8A_HUMAN	Q9h1j5 homo sapien
2	1496	73.4	354	1	WN8A_MOUSE	Q64527 mus musculu
3	1388	68.1	358	1	WN8A_XENLA	P28026 xenopus lae
4	1379	67.7	357	1	WN8C_CHICK	P51030 gallus gall
5	1316.5	64.6	359	1	WN8_BRARE	P51028 brachydanio
6	1236	60.7	350	1	WN8_MOUSE	Q9wud6 mus musculu
7	1215.5	59.7	358	1	WN8B_BRARE	Q9wud5 brachydanio
8	1213	59.5	351	1	WN8B_HUMAN	P51029 brachydanio
9	1155	56.7	428	1	WN8B_XENLA	Q93098 homo sapien
10	672.5	33.0	360	1	WN5C_XENLA	P31291 xenopus lae
11	657.5	32.3	351	1	WN4_XENLA	P33945 xenopus lae
12	656.5	32.2	359	1	WN5A_AMBME	P49338 xenopus lae
13	655.5	32.2	357	1	WN5B_PLEWA	O06442 ambystoma m
14	654.5	32.1	359	1	WN5A_AMBME	O13267 pleurodeles
15	652.5	32.0	370	1	WN1_BRARE	O06443 ambystoma m
16	650.5	31.9	391	1	WN2B_HUMAN	P24257 brachydanio
17	649.5	31.9	359	1	WN8B_HUMAN	Q93097 homo sapien
18	649.5	31.9	389	1	WN5B_HUMAN	Q9hij7 homo sapien
19	648	31.8	351	1	WN2B_MOUSE	O70283 mus musculu
20	647.5	31.8	351	1	WN4_HUMAN	P56705 homo sapien
21	646	31.7	351	1	WN4_RAT	P87387 xenopus lae
22	644	31.6	351	1	WN2B_XENLA	Q9qxg5 rattus norv
23	643.5	31.6	360	1	WN2_MOUSE	P22724 mus musculu
24	643	31.6	350	1	WN4_MOUSE	P21552 mus musculu
25	640.5	31.4	360	1	WN2_HUMAN	Q92048 brachydanio
26	640.5	31.4	380	1	WN2_BRARE	P09544 homo sapien
27	639	31.4	369	1	WN1_AMBME	P31286 xenopus lae
28	638.5	31.3	359	1	WN1_MOUSE	P21551 ambystoma m
29	637	31.3	351	1	WN4_CHICK	P22726 mus musculu
30	636.5	31.2	363	1	WN5B_BRARE	P49337 gallus gall
31	636.5	31.2	365	1	WN5_BRARE	Q92050 brachydanio
32	636	31.2	370	1	WN1_HUMAN	P41221 homo sapien
33	636	31.2	370	1	WN1_MOUSE	P04628 homo sapien
34	635	31.2	352	1	WN3A_XENLA	P04426 mus musculu
35	634.5	31.1	371	1	WN5B_ORYLA	P31285 xenopus lae
36	632	31.0	363	1	WN5_HALRO	O42122 oryzias lat
37	629	30.9	352	1	WN3A_MOUSE	O15978 halocynthia
38	628	30.8	379	1	WN3A_RAT	P27467 mus musculu
39	626	30.7	355	1	WN3_HUMAN	Q9gxq7 rattus norv
40	626	30.7	352	1	WN3_MOUSE	P56703 homo sapien
41	625	30.7	352	1	WN5A_HUMAN	P17553 mus musculu
42	623	30.6	379	1	WN5A_MOUSE	P56704 homo sapien
43	619.5	30.4	349	1	WN7B_HUMAN	P22725 mus musculu
44	617.5	30.3	349	1	WN7B_MOUSE	P28047 mus musculu
45	615.5	30.2	371	1	WN1_XENLA	P56706 homo sapien
						P10108 xenopus lae

ALIGNMENTS

RESULT 1
WN8A_HUMAN

WN8A_HUMAN

ID   WN8A_HUMAN   STANDARD;   PRT;   355 AA.
AC   Q9H1J5; Q96SS1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Wnt-8a protein precursor (Wnt-8d).
GN   WNT8A OR WNT8D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Testa T.T., Mosakowska D.E., Carter P.S., Hu E., Zhu Y.,
RA   Kelsell D.P., Murdock P.R., Herrity N.C., Lewis C.J., Cross D.A.,
RA   Culbert A.A., Reith A.D., Barnes M.R.;
RT   "Molecular cloning and characterization of six novel human WNT
RT   genes.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Saitoh T., Katoh M.;
RT   "Molecular cloning and characterization of human WNT8A.";
RL   Int. J. Oncol. 19:123-127(2001).
CC   -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC   TRANSMEMBRANE RECEPTORS. MAY PLAY AN IMPORTANT ROLE IN THE
CC   DEVELOPMENT AND DIFFERENTIATION OF CERTAIN FOREBRAIN STRUCTURES,
CC   NOTABLY THE HIPPOCAMPUS.
CC   -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC   extracellular matrix.
CC   -!- SIMILARITY: Belongs to the Wnt family.
CC   ---
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---
DR   EMBL; AB057725; BAB60960.1; -.
DR   EMBL; AY009402; AAG38662.1; -.
DR   Genew; HGNC:12788; WNT8A.
DR   MIM; 606360; -.
DR   InterPro; IPR005817; Wnt.
DR   InterPro; IPR005816; Wnt_grthfactor.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.
DR   PROSITE; PS00246; WNT1; 1.
DR   PROSITE; PS00247; WNT1; 1.
KW   Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT   SIGNAL   1   19   POTENTIAL.
FT   CHAIN   20   355   WNT-8A PROTEIN.

FT   CARBOHYD   103   103   N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD   262   262   N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD   281   281   N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CONFLICT   348   355   RVWFGVYI -> KGSA (IN REF. 1).
SQ   SEQUENCE   355 AA; 39527 MW; 605B1D5DD755FBD6 CRC64;

Query Match   87.9%; Score 1791; DB 1; Length 355;
Best Local Similarity   97.9%; Pred. No. 2.1e-147;
Matches 327; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 134

Qy   153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194

Qy   213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy   273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy   333 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGK 366
            |||||||||||||||||||||||||||||||||:
Db   315 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGR 348

RESULT 2
ID   WN8A_MOUSE   STANDARD;   PRT;   354 AA.
AC   Q64527;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Wnt-8a protein precursor (Wnt-8d) (Stimulated by retinoic acid protein
DE   11) (Wnt-8).
GN   WNT8A OR WNT8D OR STRA11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97042052; PubMed=8887323;
RA   Bouillet P., Oulad-Abdelghani M., Ward S.J., Bronner S., Chambon P.,
RA   Dolle P.;
RT   "A new mouse member of the Wnt gene family, mWnt-8, is expressed
RT   during early embryogenesis and is ectopically induced by retinoic
RT   acid.";
RL   Mech. Dev. 58:141-152(1996).
-!- FUNCTION: Ligand for members of the frizzled family of seven
     transmembrane receptors. Probable developmental protein. May be a
     signaling molecule which affects the development of discrete
     regions of tissues. Is likely to signal over only few cell
     diameters (By similarity).
-!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
     extracellular matrix.
-!- DEVELOPMENTAL STAGE: EXPRESSION IN EARLY STAGES OF EMBRYOGENESIS.
     EXPRESSION BEGINS IN THE POSTERIOR REGION OF EARLY PRIMITIVE
     STREAK-STAGE EMBRYOS AND AFTER IT SPREADS INTO THE EMBRYONIC
     ECTODERM UP TO A SHARP ROSTRAL BOUNDARY AT THE BASE OF THE
     DEVELOPING HEADFOLDS. EXPRESSED TRANSIENTLY IN THE NEWLY FORMED
     MESODERM. EXPRESSION IS DOWN-REGULATED DURING SOMITOGENESIS AND
     EXPRESSION IS HIGHLY RESTRICTED DURING GASTRULATION AND

CC   NEURULATION, BOTH TEMPORALLY AND SPATIALLY.
CC   -!- INDUCTION: By retinoic acid.
CC   -!- SIMILARITY: Belongs to the Wnt family.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; 268889; CAA93117.1; -.
DR   MGD; MGI:1079924; Wnt8a.
KW   Wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT   SIGNAL   1   19   POTENTIAL.
FT   CHAIN   20   354   WNT-8A PROTEIN.
FT   CARBOHYD   103   103   N-LINKED (GLCNAC...)   (POTENTIAL).
FT   CARBOHYD   262   262   N-LINKED (GLCNAC...)   (POTENTIAL).
SQ   SEQUENCE   354 AA; 39473 MW; 1CA65E83840184D9 CRC64;

Query Match   73.4%; Score 1496; DB 1; Length 354;
Best Local Similarity   82.5%; Pred. No. 6.4e-122;
Matches 269; Conservative 22; Mismatches 35; Indels 0; Gaps 0;

Qy   42 SVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATR 101
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   24 SVNNFLITGPKAYLTYTTAASVALGAQSGIEECKFQFAWERWNCPEHAFQFSTHNRLRAATR 83

Qy   102 ETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERIS 161
            |||||||:|| ||||||||||||||||||||||||||||||||||||||||:||
Db   84 ETSFIHAIRSAAIMYAVTKNCSMGDLENCGCDGESQNGKTGGHGWIWGGCSDNVEFGEKIS 143

Qy   162 KLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE 221
            |||||||||||||||||||||||||||||||||:||||||:|||| ||||||||||
Db   144 RLFVDSLEKGKDARALVNLHNNRAGRLAVRASTKRTCKCHGISGSCSIQTCWLQLADFRQ 203

Qy   222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNS 281
            ||:|||||||:||||||||||||||||:|||| |||||||:||| |:|||||||||
Db   204 MGNYLKAKYDRALKIEMDKRQLRAGNRAEGRWALTEAFLPSTEAEILFLEGSPDYCNRNA 263

Qy   282 SLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVK 341
            ||||||||||||||:|| ||||||||||||||||||||:||||||||||:|||||||||
Db   264 SLSIQGTEGRECLQNARSASRREQRSCGRLCTECGLQVERRAEAVSSCDCDNFQWCCTVK 323

Qy   342 CDQCRHVVSKYYCARSPGSAQSLGKG 367
            |||||||:|| ||||||: || :|
Db   324 CGQCRRVVSRYYCTRPVGSARPRGRG 349

RESULT 3
ID   WN8_XENLA   STANDARD;   PRT;   358 AA.
AC   P28026;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Wnt-8 protein precursor (XWnt-8).
GN   WNT-8.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91347916; PubMed=1879349;

OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

Run on: January 30, 2004, 13:26:30 ; Search time 41 Seconds
2322.473 Million cell updates/sec
(without alignments)

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCCIQCLCLVSPFPTLTPC..........SKYYCARSPGSAQSIGKGSA 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungi1:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacterial:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1415	69.5	381		Q90ZA3	ambystoma m
2	1266	62.2	354	13	Q90XK5	rattus norv
3	1266	62.2	354	13	Q90YL8	brachydanio
4	1243	61.0	368	13	Q90YJ8	brachydanio
5	994.5	48.8	362	11	Q8BQD1	mus musculu
6	978	48.0	364	5	Q9U416	branchiosto
7	676.5	33.2	315	5	Q9NCP9	branchiosto
8	676.5	33.2	385	13	Q9PUI3	gallus gall
9	661.5	32.5	381	5	Q9PUI3	gallus gall
10	656	32.2	387	13	Q98SN7	gallus gall
11	651	32.0	351		Q8T395	cuplennius
12	650.5	31.9	311	11	Q81UM6	homo sapien
13	647.5	31.8	360	11	Q9QXK5	rattus norv
14	647.5	31.8	360	11	Q9CZW3	mus musculu
15	638.5	31.3	372	11	Q91XF5	mus musculu
16	637.5	31.3	374	5	Q8T396	cuplennius
17	636.5	31.2	360	11	Q8bm17	mus musculu
18	636.5	31.2	380	11	Q8vcv6	mus musculu
19	635.5	31.2	370	13	P79752	fugu rubrip
20	633	31.1	370	5	Q8ws75	branchiosto
21	633	31.1	376	13	Q9pwh1	gallus gall
22	632.5	31.1	353	5	Q9tzt6	branchiosto
23	632.5	31.1	371	5	Q8t8a8	halocynthia
24	632.5	31.1	380	11	Q8bmf9	mus musculu
25	629.5	30.9	385	13	Q9ygx6	gallus gall
26	626	30.7	329	11	Q8bli2	mus musculu
27	619.5	30.4	349	13	Q42258	xenopus lae
28	618	30.3	350	13	Q9u6v0	ciona intes
29	617	30.3	377	13	Q8uw39	fugu rubrip
30	617	30.3	394	5	Q61699	branchiosto
31	611.5	30.0	377	5	Q9gra6	gryllus bim
32	610.5	30.0	364	11	Q61700	branchiosto
33	609	29.9	352	5	Q8c6p4	mus musculu
34	609	29.9	270	5	Q9v584	drosophila
35	607.5	29.8	375	5	Q8mpl3	platyneteis
36	606.5	29.8	349	5	Q8mpl6	platyneteis
37	606	29.6	375	5	Q9deb8	gallus gall
38	602.5	29.6	358	13	Q8deb8	gallus gall
39	601	29.5	349	11	Q9iau3	platyneteis
40	600.5	29.5	349	11	Q96h90	homo sapien
41	599.5	29.4	363	5	Q9dby3	mus musculu
42	597	29.3	358	5	Q9gtj9	hydra atten
43	594.5	29.2	331	5	Q8mpl8	platyneteis
44	593	29.1	415	5	Q8ipi1	drosophila
45	589	28.9	365	4	Q8n2e5	homo sapien

ALIGNMENTS

RESULT 1
Q90ZA3

ID   Q90ZA3   PRELIMINARY;   PRT;   381 AA.
AC   Q90ZA3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Secreted factor Axwnt-8.
GN   WNT-8.
OS   Ambystoma mexicanum (Axolotl).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC   Ambystoma.
OX   NCBI_TaxID=8296;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bachvarova R.F., Masi T., Thomas J., Hall L., Johnson A.D.;
RT   "Formation of posterior ventrolateral mesoderm in the urodele,
RT   Ambystoma mexicanum: expression of Axbra and Axwnt-8.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC   EXTRACELLULAR MATRIX (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
DR   EMBL; AF308871; AAK58845.1; -.
DR   InterPro; IPR005817; -.
DR   InterPro; IPR005816; Wnt.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.
DR   PROSITE; PS00246; WNT1; 1.
KW   Developmental protein; Glycoprotein.
SQ   SEQUENCE   381 AA; 42728 MW; 6A392F9C15FA64F4 CRC64;

Query Match   69.5%;   Score 1415;   DB 13;   Length 381;
Best Local Similarity 75.9%;   Pred. No. 3.8e-130;
Matches 246; Conservative   41; Mismatches 37; Indels   0; Gaps   0;

Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92

RESULT 2

```
Q90YL8

ID   Q90YL8      PRELIMINARY;      PRT;    354 AA.
AC   Q90YL8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Wnt8-like protein 2.
GN   WNT8.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;
RT   "Zebrafish wnt8 encodes two Wnt8 proteins on a bicistronic transcript
RT   and is required for mesoderm and neurectoderm patterning.";
RL   Dev. Cell 1:0-0(2001).
DR   EMBL; AY032749; AAK70224.1; -.
DR   InterPro; IPR005817; Wnt.
DR   InterPro; IPR005816; Wnt_grthfactor.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.
SQ   SEQUENCE   354 AA;  40109 MW;  F42951A27AC38A67 CRC64;

Query Match             62.2%;  Score 1266;  DB 13;  Length 354;
Best Local Similarity   69.0%;  Pred. No. 1.4e-115;
Matches  220;  Conservative  44;  Mismatches  55;  Indels  0;  Gaps  0;
```

```
Db   16 CTIFTASAWSVNNFLMTGPKAYLTYSTSVAVGAQOSGIEECKFQFAWERWNCPESALQLST 75
Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCCSD 152
Db  136 NVDFGERISKPFVDALETGQDSRALMNIHNNEAGRFAVKSTMKRTCKCHGVSGSCSIQTC 195
Qy   76 HNGLRSATRETSFVHAISSAGVMYTLTRNCSMGDFDNCGCGDDSRNGRMGGRGWVWGGCSD 135
Db  153 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 212
Qy  136 NVDFGERISKPFVDALETGQDSRALMNIHNNEAGRFAVKSTMKRTCKCHGVSGSCSIQTC 195
Db  256 SPDYCLRNASLGLQGTEGRECLQSGKNLSQWEKRSCRRLCTECGLKVEERKTEIVSSCNC 315
Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
Db  196 WLQLAEFRDIGNYLKIKHDQALKLEMDKRRMRAGNSADNRGAIAEAFSSLVATELIFLED 255
Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
Db  256 SPDYCLRNASLGLQGTEGRECLQSGKNLSQWEKRSCRRLCTECGLKVEERKTEIVSSCNC 315
Qy  333 KFQWCCTVKCDQCRHVVSKYYCAR 356
Db  316 KFHWCCTVKCEQCRQVVTKHYCAR 339
```

RESULT 3

```
Q90YJ8

ID   Q90YJ8      PRELIMINARY;      PRT;    354 AA.
AC   Q90YJ8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Wnt8-like protein 2.
GN   WNT8.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;
RT   "Zebrafish wnt8 encodes two Wnt8 proteins on a bicistronic transcript
RT   and is required for mesoderm and neurectoderm patterning.";
RL   Dev. Cell 1:0-0(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Lekven A.C., Thorpe C.J., Waxman J.S., Moon R.T.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U10869; AAK68628.1; -.
DR   ZFIN; ZDB-GENE-980526-332; wnt8.
DR   InterPro; IPR005817; Wnt.
DR   InterPro; IPR005816; Wnt_grthfactor.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.
SQ   SEQUENCE   354 AA;  40065 MW;  B25CEDFB7453FD37 CRC64;

Query Match             62.2%;  Score 1266;  DB 13;  Length 354;
Best Local Similarity   69.0%;  Pred. No. 1.4e-115;
Matches  220;  Conservative  44;  Mismatches  55;  Indels  0;  Gaps  0;
```

```
Qy   42 SVNNFLITGPKAYLTYTTSVALGAQOSGIEECKFQFAWERWNCPENALQLSTHNRLRSATR 101
Db   24 TMNNLLITGPRAYLITYANSVRVGAQOSGIHECKHQFAWDRWNCPDTALQLSTHKGLRSATR 83
Qy  102 ETSFIHAISSAGVMYIIITKNCSMGDFENCGCGDGSNNGKTGGHGWIWGGCCSDNVEFGERIS 161
Db   84 ESSFVHAISAGVMYTLTRNCSLGDLNECGCDSSRNGRLGGRGWLWGGCSDNVDFGERIS 143
Qy  162 KLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE 221
Db  144 KQFVDALETGQDARAAVNLHNNEAGRLAVKATMKR.CRCHGMSESCTMQTCWMQLADFRE 203
Qy  222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAEIIFLEESPDYTCNS 281
Db  204 IGNYLKVKHDQAKLEMDKRRMRAGNSADNRVTMTDAFGSIARTELIYLEDSPDYCAKNL 263
Qy  282 SLGIGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVK 341
Db  264 SLGLPGTEGRECVQHGESLSQWERRSCRRLCHECGLRVEERRTEVVSSCNCKFHWCCTVK 323
Qy  342 CDQCRHVVSKYYCARSPGS 360
Db  324 CENCSQVTVKHVCTRRHGS 342
```

RESULT 4

```
Q8BQD1

ID   Q8BQD1      PRELIMINARY;      PRT;    368 AA.
```

OM protein - protein search, using sw model

Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 13:27:50 ; Search time 21 Seconds
                                               (without alignments)
                                               743.462 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCCIQCLCLVSPFPTITPC...........SKYYCARSPGSAQSLGKGSA 369

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum Match length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents AA:*
            1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
            2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
            3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
            4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
            5: /cgn2_6/ptodata/1/1aa/pCTUS_COMB.pep:*
            6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	640.5	360	4	US-09-417-039-4	Sequence 4, Appli
2	636.5	360	4	US-09-417-039-4	Sequence 4, Appli
3	636.5	365	3	US-09-067-782A-2	Sequence 9, Appli
4	636	351	3	US-09-067-782A-2	Sequence 2, Appli
5	636	370	4	US-09-417-039-3	Sequence 3, Appli
6	634.5	359	4	US-09-082-089-3	Sequence 3, Appli
7	634.5	363	3	US-09-082-089-5	Sequence 5, Appli
8	634.5	372	3	US-09-082-089-2	Sequence 2, Appli
9	626	355	3	US-09-082-270-2	Sequence 2, Appli
10	620.5	397	1	US-08-647-928-8	Sequence 8, Appli
11	600.5	349	3	US-09-459-774-2	Sequence 2, Appli
12	600.5	349	4	US-09-903-87-2	Sequence 2, Appli
13	593.5	349	4	US-09-417-039-7	Sequence 7, Appli
14	531.5	389	2	US-08-485-449-7	Sequence 7, Appli
15	528.5	389	2	US-08-485-449-6	Sequence 6, Appli
16	487	376	2	US-08-485-449-5	Sequence 5, Appli
17	370.5	159	4	US-09-082-270-4	Sequence 4, Appli
18	268	133	4	US-09-417-039-5	Sequence 5, Appli
19	222	121	4	US-09-067-782A-5	Sequence 5, Appli
20	216	120	4	US-09-417-039-6	Sequence 6, Appli
21	209	124	4	US-09-417-039-8	Sequence 8, Appli
22	155	131	4	US-09-067-782A-4	Sequence 4, Appli
23	104	788	2	US-08-918-914-4	Sequence 4, Appli
24	101	1193	2	US-08-400-159-10	Sequence 10, Appl
25	101	1193	3	US-08-611-729A-10	Sequence 10, Appl
26	99.5	1193	3	US-08-872-855-10	Sequence 10, Appl
27	97	24	3	US-08-726-867A-10	Sequence 10, Appl
28	97	24	3	US-08-942-806A-10	Sequence 10, Appl
29	96.5	1184	2	US-08-918-914-1	Sequence 1, Appli
30	96.5	1184	3	US-08-996-083-3	Sequence 3, Appli
31	95	488	1	US-08-243-542-1	Sequence 1, Appli
32	95	488	1	US-08-477-407-1	Sequence 1, Appli
33	95	488	1	US-08-484-355-1	Sequence 1, Appli
34	95	524	1	US-08-243-542-2	Sequence 2, Appli
35	95	524	1	US-08-477-407-2	Sequence 2, Appli
36	95	524	1	US-08-484-355-2	Sequence 2, Appli
37	95	670	1	US-08-243-542-3	Sequence 3, Appli
38	95	670	1	US-08-477-407-3	Sequence 3, Appli
39	95	670	1	US-08-484-355-3	Sequence 3, Appli
40	95	769	1	US-08-243-542-4	Sequence 4, Appli
41	95	769	1	US-08-477-407-4	Sequence 4, Appli
42	95	769	1	US-08-484-355-4	Sequence 4, Appli
43	95	1010	3	US-08-882-046-7	Sequence 7, Appli
44	95	1036	4	US-09-068-740A-6	Sequence 6, Appli
45	95	1187	4	US-09-068-740A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-417-039-4

; Sequence 4, Application US/09417039A
; Patent No. 6485972
; GENERAL INFORMATION:
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Parr, Brian A.
; APPLICANT: Vainio, Seppo
; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS
; FILE REFERENCE: 00246/232001
; CURRENT APPLICATION NUMBER: US/09/417,039A
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 60/109,355
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-039-4

  Query Match   31.4%; Score 640.5; DB 4; Length 360;
  Best Local Similarity   40.8%; Pred. No. 5.1e-58;
  Matches 125; Conservative 54; Mismatches 108; Indels 19; Gaps 7;

Qy   60 SVALGAQSGIEECKFQFAWERWNCPENALQLSTHNR-LRSATRETSFIHAISSAGYMYII 118
                   ::: |||||||||||||||||||||||||| ::||||||||||||||||
Db   64 AISQGVAEWTAECQHQFPRQHRWNCNTLDRDHSLFGRVLLRSSRESAPVYAISSAGVVFAI 123

Qy   119 TKNCSMGDFENCGCDGSNNGKTGGHGWI---WGGCSDNVEFGERISKLFVDSLE-KGKDAR 175
                :::||:| :|||| || || |||| |||::::||| :|||::||:: ||||
Db   124 TRACSQGEVKSCSCCDPKKMGSAKDSKGIFDWGGCSDNIDYGIKFARAFVDAKERKGKDAR 183

Qy   176 ALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALK 235
                 ||||:|||||| ||: ||||||||||| |||||| ||| ||:| ::|||| ||:||
Db   184 ALMNLHNNRAGRKAVKRFLKQQECKCHGVSGSCTLRTCWLAMADFRKTGDYLWRKYNGAIQ 243

Qy   236 IEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECLQ 295
                ||||::| ||||::|| || :|| | :||||||||:||:|:|||::||:|||| :| :
Db   244 VVMNQ--------DGTGFTVANERFKKPTKNDLVYFENSPDYCIRDREAGSLGTAGRVCNL 296

Qy   296 NSHNTSRWERRSCGRLCTECGLQVEERKIEVISSCNCKFQWCCTVKCDQCRHVSKYYCA 355
                :::|:::||:::|||||:||||:|||| :: :::: | : ||||||:|:|:: ::|:
Db   297 TSRGMD------SCEVMC--CGRGYDTSHVTRMTKCGCKFHWCCAVRCQDCLEALDVHTC- 348

Qy   356 RSPGSA 361
                :| :|
Db   349 KAPKNA 354

RESULT 2
US-09-417-039-9
; Sequence 9, Application US/0941703A
; Patent No. 6485972
; GENERAL INFORMATION:
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Parr, Brian A.
; APPLICANT: Vaino, Seppo
; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS
; FILE REFERENCE: 00246/232001
; CURRENT APPLICATION NUMBER: US/09/417,039A
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 60/109,355
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-039-9

Query Match   31.2%;   Score 636.5; DB 4;   Length 365;
Best Local Similarity 40.2%;   Pred. No. 1.4e-57;
Matches 125; Conservative 52; Mismatches 107; Indels 27; Gaps 8;

Qy   54 YLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNR-LRSATRETSFIHAISSA 112
              : ||: ||.||:||.||||||||||||||||||||||: || |||.|.|| .|||
Db   71 YQDHMQYIGEGAKTGIKECQYQFRHRRWNC-STVDNTSVFGRVMQIGSRETAFTYAVSAA 129

Qy   113 GVMYIITKNCSMGDFENCGCDGSNNGKTGHGWIWGGCSDNVEFGERISKLFVDSLE--- 169
              ||: |||||||||||||||||||||||||||||||||.|||||||||||||||
Db   130 GVNNAMSRACREGELSTCGCSRAARPKDLPRDWLMGGCGDNIDYGYRFAKEFVDARERER 189

Qy   170 ---KG--KDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGD 224
              || ||||||||||||||||||||||||||||||||||||||||||.|||:|:
Db   190 IHAKGSYESARILLMNLHNNEAGRRTVNLADVACKCHGVSGSCSLKTCWLQLADFRKVGD 249

Qy   225 YLKAKYDQALKIEMDKR-QLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSL 283
              ||||.||.||||||: ||||.||||.||:|||.:|:||||||||||:||||||||
Db   250 ALKEKYDSAAAMRLNSRGKLVQVNS------------RFNSPTTQDLLVIIDPSPDYCVRNEST 300

Qy   284 GIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCD 343
              : ||||:||:||||||||||||||||||||:||||||||||||||||:|:||||:||
Db   301 GSLGTQGRLCNKTSEGMD-----GCELMC--CGRGYDQFKTVQTERCHCKFHWCCVVKCK 353

Qy   344 QCRHVVSKYYC 354
              |:| |||:||
Db   354 KCTEIVDQFVC 364

RESULT 3
US-09-067-782A-2
; Sequence 2, Application US/0906778A
; Patent No. 6165751
; GENERAL INFORMATION:
; APPLICANT: BARNES, MICHAEL
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: US
; ZIP: 19482-0980
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/067,782A
; FILING DATE: 28-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 9710734.6
; FILING DATE: 23-MAY-1997
; APPLICATION NUMBER: EP 97309144.0
; FILING DATE: 13-NOV-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30167
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 601-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-067-782A-2

Query Match   31.2%;   Score 636; DB 3;   Length 351;
Best Local Similarity 37.9%;   Pred. No. 1.4e-57;
Matches 139; Conservative 49; Mismatches 119; Indels 60; Gaps 11;

Qy   26 CLIPIHLCLTFSLFGRSVNNFLIIGP----------------------------KAYLIYT 58
              ||:|:|:|| ::| .|||.
Db   6 CLRSLRL-LVFAVFSAAASNWLYLAKLSSVGSISEETCEKLLKGLIQRQVQMCKRNLEVM 64

Qy   59 TSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRL------RSATRETSFIHAISS 111
              |||||.:||: ||: |:| ::||||||.||:|||
Db   6 DSVRRGAQLAIEECQYQFRNRRWNC------STLDSLPVFGKVVTQGIREAALVYAISS 117

Qy   112 AGVMYIITKNCSMGDFENCGCDGSNNGKTGHGWIWGGCSDNVEFGERISKLFVDSLEKG 171
              ||||||||||.|||:||||||||.|| ||.||:.||:||||||||||||||
Db   118 AGVAFAVTRACSSGELEKCCGCDRTVHG-VSPQGFOWSGCSDNIAYGVAFSQSFVDVRERS 176

Qy   172 KDA--RALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKA 228
              || |||||||||.||| |:|.:|||||||:|:||||:||||||||.||:|
Db   177 KGASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPRQVGHALKE 236

Qy   229 KYDQALKIEMDKRQLRAGNSAEGHWVPAEA-FLPSAEAELIFLEESPDYCTCNSSLGIYG 287
              ||||||||||| :||:| ||||.|||||| ||||||||||||||||||||:||||.
Db   237 KFDGATEVE-----PRRVGSSRA--LVPRNAQFKPHTDEDLIVYLEPSPDFCEQDMRSGVLG 290

Qy   288 TEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDCDRH 347
              ||||||.||||||:|||||||||||||||::||||||||||||||||||||:||: :|
Db   291 TRGRTCNKTSKAID------GCELLC--CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQR 343

Qy   348 VVSKYYC 354
              ::.||
Db   344 LVELHTC 350

RESULT 4
US-09-417-039-3
; Sequence 3, Application US/0941703A
; Patent No. 6485972
; GENERAL INFORMATION:
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Parr, Brian A.
; APPLICANT: Vaino, Seppo
; TITLE OF INVENTION: WNT SIGNALLING IN REPRODUCTIVE ORGANS
; FILE REFERENCE: 00246/232001
; CURRENT APPLICATION NUMBER: US/09/417,039A
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 60/109,355
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 11
;

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 13:30:11 ; Search time 40 seconds
                                       (without alignments)
                                       1917.177 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCCIQCLCLVSPFPTLTPC..........SKYYCARSPGSAQSLGKGSA 369

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
     1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
     2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
     3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
     4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
     5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
     6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
     7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
     8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
     9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
    10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
    11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
    12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
    13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
    14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
    15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
    16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
    17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
    18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1808	88.8	351	12	US-10-275-115-2	Sequence 2, Appli
2	1802	88.5	351	11	US-09-842-758-8	Sequence 8, Appli
3	1791	87.9	355	11	US-09-842-758-44	Sequence 44, Appli
4	1791	87.9	355	12	US-10-285-976-23	Sequence 23, Appli
5	1783	87.5	415	14	US-10-005-947-2	Sequence 2, Appli
6	1496	73.4	354	11	US-09-842-758-45	Sequence 45, Appli
7	1496	73.4	354	14	US-10-005-947-4	Sequence 4, Appli
8	1388	68.1	387	11	US-09-842-758-46	Sequence 46, Appli
9	1379	67.7	357	11	US-09-842-758-47	Sequence 47, Appli
10	1211	59.5	351	12	US-10-285-976-25	Sequence 25, Appli
11	1137.5	55.8	295	14	US-10-005-947-6	Sequence 6, Appli
12	973	47.8	176	12	US-10-029-386-32775	Sequence 32775, A
13	712	35.0	352	12	US-10-028-248A-71	Sequence 71, Appl
14	649.5	31.9	359	12	US-10-285-976-15	Sequence 15, Appl
15	649.5	31.9	359	12	US-10-295-027-584	Sequence 584, App
16	648	31.8	351	10	US-09-978-295A-226	Sequence 226, App
17	648	31.8	351	10	US-09-978-697-226	Sequence 226, App
18	648	31.8	351	10	US-09-978-192A-226	Sequence 226, App
19	648	31.8	351	10	US-09-999-832A-226	Sequence 226, App
20	648	31.8	351	11	US-09-978-189-226	Sequence 226, App
21	648	31.8	351	11	US-09-978-608A-226	Sequence 226, App
22	648	31.8	351	11	US-09-978-585A-226	Sequence 226, App
23	648	31.8	351	11	US-09-978-191A-226	Sequence 226, App
24	648	31.8	351	11	US-09-978-403A-226	Sequence 226, App
25	648	31.8	351	11	US-09-978-564A-226	Sequence 226, App
26	648	31.8	351	11	US-09-999-833A-226	Sequence 226, App
27	648	31.8	351	11	US-09-981-915A-226	Sequence 226, App
28	648	31.8	351	11	US-09-978-824-226	Sequence 226, App
29	648	31.8	351	11	US-09-918-585A-226	Sequence 226, App
30	648	31.8	351	11	US-09-978-193A-226	Sequence 226, App
31	648	31.8	351	11	US-09-978-423A-226	Sequence 226, App
32	648	31.8	351	11	US-09-999-830A-226	Sequence 226, App
33	648	31.8	351	11	US-09-978-757A-226	Sequence 226, App
34	648	31.8	351	11	US-09-978-187B-226	Sequence 226, App
35	648	31.8	351	11	US-09-978-643A-226	Sequence 226, App
36	648	31.8	351	11	US-09-978-375A-226	Sequence 226, App
37	648	31.8	351	11	US-09-978-188A-226	Sequence 226, App
38	648	31.8	351	12	US-09-978-298A-226	Sequence 226, App
39	648	31.8	351	11	US-10-143-031A-226	Sequence 226, App
40	648	31.8	351	12	US-10-143-031A-226	Sequence 226, App
41	648	31.8	351	12	US-10-002-967A-226	Sequence 226, App
42	648	31.8	351	12	US-10-017-083A-226	Sequence 226, App
43	648	31.8	351	12	US-10-143-030A-226	Sequence 226, App
44	648	31.8	351	12	US-09-199-672-80	Sequence 80, Appl
45	648	31.8	351	12	US-10-187-749-80	Sequence 80, Appl
	648	31.8	351	12	US-10-194-457-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-10-275-115-2
; Sequence 2, Application US/10275115
; Publication NO. US20030175805A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New wingless gene Wnt-8D
; FILE REFERENCE: WNT8dKDWS
; CURRENT APPLICATION NUMBER: US/10/275,115
; CURRENT FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-275-115-2

Query Match   88.8%; Score 1808; DB 12; Length 351;
Best Local Similarity   98.2%; Pred. No. 1.2e-168;
Matches 331; Conservative   0; Mismatches   6; Indels   0; Gaps   0;

Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKPQFAWERWNCPENALQLST 92
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 134

Qy   153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194

Qy   213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHHVPAEAFLPSAEABLIFLEE 272
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHHVPAEAFLPSABABLIFLEE 254

```
Qy    273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy    333 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 369
          |||||||||||||||||||||||||||||||||||||
Db    315 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 351
```

RESULT 2
US-09-842-758-8
; Sequence 8, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tcherney, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Esha A
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US2003008244A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,591
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; PRIOR FILING DATE: 2001-01-30
; SOFTWARE: Patentin Ver. 2.1
; NUMBER OF SEQ ID NOS: 113
; SEQ ID NO 8
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-842-758-8
; Sequence 44, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:

Query Match 88.5%; Score 1802; DB 11; Length 351;
Best Local Similarity 97.9%; Pred. No. 4.7e-168;
Matches 330; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy     33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
          |||  |  |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     15 CAAFSASAWVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy     93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db     75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKIGGHGWIWGGCSD 134

Qy    153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194

Qy    213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy    273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy    333 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 369
          |||||||||||||||||||||||||||||||||||||
Db    315 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 351
```

RESULT 3
US-09-842-758-44
; Sequence 44, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shimkets, Richard A
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tcherney, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Esha A
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US2003008244A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
```

```
;   PRIOR APPLICATION NUMBER: 60/201,238
;   PRIOR FILING DATE: 2000-05-01
;   PRIOR APPLICATION NUMBER: 60/201,186
;   PRIOR FILING DATE: 2000-05-02
;   PRIOR APPLICATION NUMBER: 60/201,474
;   PRIOR FILING DATE: 2000-05-03
;   PRIOR APPLICATION NUMBER: 60/201,508
;   PRIOR FILING DATE: 2000-05-03
;   PRIOR APPLICATION NUMBER: 60/220,591
;   PRIOR FILING DATE: 2000-07-25
;   PRIOR APPLICATION NUMBER: 60/232,678
;   PRIOR FILING DATE: 2000-09-15
;   PRIOR APPLICATION NUMBER: 60/263,217
;   PRIOR FILING DATE: 2001-01-22
;   PRIOR APPLICATION NUMBER: 60/265,160
;   PRIOR FILING DATE: 2001-01-30
;   NUMBER OF SEQ ID NOS: 113
;   SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 44
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens

US-09-842-758-44

  Query Match             87.9%;  Score 1791;  DB 11;  Length 355;
  Best Local Similarity   97.9%;  Pred. No. 5.7e-167;
  Matches  327;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
            |   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy    93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 134

Qy   153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194

Qy   213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy   273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy   333 KPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGK 366
         |||||||||||||||||||||||||||||||||:
Db   315 KPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGR 348


RESULT 4
US-10-285-976-23

;   Sequence 23, Application US/10285976
;   Publication No. US20030165500A1
;   GENERAL INFORMATION:
;     APPLICANT: Rhee, Chae-Seo
;     APPLICANT: Malini, Sen
;     APPLICANT: Wu, Christina
;     APPLICANT: Leoni, Lorenzo M.
;     APPLICANT: Corr, Maripat
;     APPLICANT: Carson, Dennis A.
;     TITLE OF INVENTION: The Regents of the University of California
;     TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
;     TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
;     FILE REFERENCE: 023070-13032US
;     CURRENT APPLICATION NUMBER: US/10/285,976
;     CURRENT FILING DATE: 2002-11-01
;     PRIOR APPLICATION NUMBER: US 60/287,995
;     PRIOR FILING DATE: 2001-05-01
;     PRIOR APPLICATION NUMBER: WO PCT/US02/13802
```

```
;     PRIOR FILING DATE: 2002-05-01
;     NUMBER OF SEQ ID NOS: 232
;     SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 23
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human Wnt-8a

US-10-285-976-23

  Query Match             87.9%;  Score 1791;  DB 11;  Length 355;
  Best Local Similarity   97.9%;  Pred. No. 5.7e-167;
  Matches  327;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
            |   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy    93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 134

Qy   153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194

Qy   213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy   273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy   333 KPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGK 366
         |||||||||||||||||||||||||||||||||:
Db   315 KPQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGR 348


RESULT 5
US-10-005-947-2

;   Sequence 2, Application US/10005947
;   Publication No. US20020123103A1
;   GENERAL INFORMATION:
;     APPLICANT: Holloway, James L.
;     TITLE OF INVENTION: Human Wnt Gene
;     FILE REFERENCE: 99-87
;     CURRENT APPLICATION NUMBER: US/10/005,947
;     CURRENT FILING DATE: 2001-12-03
;     PRIOR APPLICATION NUMBER: US/09/715,993
;     PRIOR FILING DATE: 2000-11-17
;     NUMBER OF SEQ ID NOS: 6
;     SOFTWARE: FastSEQ for Windows Version 3.0
;
;   SEQ ID NO 2
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens

US-10-005-947-2

  Query Match             87.5%;  Score 1783;  DB 14;  Length 415;
  Best Local Similarity   98.2%;  Pred. No. 4.3e-166;
  Matches  326;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
            |   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 74

Qy    93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 152
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSD 134

Qy   153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
```

Db 135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194
Qy 213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
Db 195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254
Qy 273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
Db 255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314
Qy 333 KFPQWCCTVKCDQCRHVVSKYYCARSPGSAQSL 364
Db 315 KFPQWCCTVKCDQCRHVVSKYYCARSPGSAQSL 346

; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 45
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-842-758-45

Query Match   73.4%; Score 1496; DB 11; Length 354;
Best Local Similarity   82.5%; Pred. No. 4.7e-138;
Matches 269; Conservative 22; Mismatches 35; Indels   0; Gaps   0;

Qy   42 SVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATR 101
Db   24 SVNNFLITGPKAYLTYTASVALGAQIGIEECKFQFAWERWNCPEHAFQFSTHNRLRAATR   83
Qy 102 ETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERIS 161
Db   84 ETSFIHAIRSAAIMYAVTKNCSMGDLENCGCDESQNGKTGGHGWIWGGCSDNVEFGEKIS 143
Qy 162 KLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE 221
Db 144 RLFVDSLEKGKDARALVNLHNNRAGRLAVRASTKRTCKCHGISGSCSIQTCWLQLADFRQ 203
Qy 222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEERSPDYCTCNS 281
Db 204 MGNYLKAKYDRALKIEMDKRQLRAGNRAEGRWALTEAFLPSTEAELIFLEGSPDYCNRNA 263
Qy 282 SLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVK 341
Db 264 SLSIQGTEGRECLQNARSASRREQRSCGRLCTECGLQVEERRAEAVSSCDCNFQWCCTVK 323
Qy 342 CDQCRHVVSKYYCARSPGSAQSLGKG 367
Db 324 CGQCRVVSRYYCTRPVGSARPRGRG 349

RESULT 6
US-09-842-758-45
Sequence 45, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:
 APPLICANT: Vernet, Corine A. M.
 APPLICANT: Fernandes, Elma R
 APPLICANT: Gerlach, Valerie
 APPLICANT: Shimkets, Richard A
 APPLICANT: Malyankar, Uriel M
 APPLICANT: Boldog, Ferenc L
 APPLICANT: Zerhusen, Bryan D
 APPLICANT: Spytek, Kimberly A
 APPLICANT: Majumder, Kumud
 APPLICANT: Tchernev, Velizar T
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Patturajan, Meera
 APPLICANT: Burgess, Catherine E
 APPLICANT: Gangolli, Esha A
 APPLICANT: Smithson, Glennda
 APPLICANT: Rastelli, Luca
 APPLICANT: MacDougall, John R
 APPLICANT: Taupier, Raymond J
 APPLICANT: Grosse, William M
 APPLICANT: Edward, Szekeres S
 APPLICANT: Alsobrook II, John P
 TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 CURRENT APPLICATION NUMBER: US20030083244A1el
 FILE REFERENCE: 15966-783
 CURRENT APPLICATION NUMBER: US/09/842,758
 CURRENT FILING DATE: 2001-04-25
 PRIOR APPLICATION NUMBER: 60/200,158
 PRIOR FILING DATE: 2000-04-26
 PRIOR APPLICATION NUMBER: 60/200,613
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,780
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/201,006
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/201,007
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/201,236
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/201,238
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/201,186
 PRIOR FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: 60/201,508
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 60/201,474
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 60/220,591
 PRIOR FILING DATE: 2000-07-25
 PRIOR APPLICATION NUMBER: 60/232,678
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 60/263,217
 PRIOR FILING DATE: 2001-01-22
 PRIOR APPLICATION NUMBER: 60/265,160
 PRIOR FILING DATE: 2001-01-30

RESULT 7
US-10-005-947-4
Sequence 4, Application US/10005947
Publication No. US20020123103A1
GENERAL INFORMATION:
 APPLICANT: Holloway, James L.
 TITLE OF INVENTION: Human Wnt Gene
 FILE REFERENCE: 99-87
 CURRENT APPLICATION NUMBER: US/10/005,947
 CURRENT FILING DATE: 2001-12-03
 PRIOR APPLICATION NUMBER: US/09/715,993
 PRIOR FILING DATE: 2000-11-17
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mouse
US-10-005-947-4

Query Match   73.4%; Score 1496; DB 14; Length 354;
Best Local Similarity   82.5%; Pred. No. 4.7e-138;
Matches 269; Conservative 22; Mismatches 35; Indels   0; Gaps   0;

Qy   42 SVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATR 101
Db   24 SVNNFLITGPKAYLTYTASVALGAQIGIEECKFQFAWERWNCPEHAFQFSTHNRLRAATR   83
Qy 102 ETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERIS 161
Db   84 ETSFIHAIRSAAIMYAVTKNCSMGDLENCGCDESQNGKTGGHGWIWGGCSDNVEFGEKIS 143
Qy 162 RLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE 221
Db 144 RLFVDSLEKGKDARALVNLHNNRAGRLAVRASTKRTCKCHGISGSCSIQTCWLQLADFRQ 203

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 387
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-842-758-46

```
Query Match             68.1%;  Score 1388;  DB 11;  Length 387;
Best Local Similarity   75.3%;  Pred. No. 2.1e-127;
Matches  244;  Conservative   40;  Mismatches   40;  Indels    0;  Gaps    0;

Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST 92
           |||| ||||||| |||:|||||||:  |:|:|||||||| ||||||||:|||||||| ||:||:
Db   16 CPFFTASAWSVNNFLMTGPRAYLTYSASVAVGAQONGIEECKYQFAWERWNCPESTLQLAT 75

Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCGDGSNNGKTGHGHWIWGGCSD 152
           || ||||||||||:|||||||||||| | :||||||||| |||||:: |:||:|||||||||
Db   76 HNGLRSATRETSFVHAISSAGVMYTLTRNCSMGDFDNCGCGDDSRNGRIGGRGWVWGGCSD 135

Qy  153 NVEFGERISKLFVDSLEKGKDARALMNLHHNRAGRLAVRATMKRTCKHCGISGSCSIQTC 212
           | |||||||||||||:||:||:|||||||||||| ||||  :|||||||||||||||||||||
Db  136 NAEFGERISKLFVDGLETGQDARALMNLHHNEAGRLAVKETMKRTCKHCGISGSCSIQTC 195

Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
           ||||||||: ||:||| ||||||:|||||||:||||||:||    |||||||||||||||||:
Db  196 WLQLAEFRDIGNHLKLKHDQALKLEMDKRKMRSGNSADNRGAIADAFSSVAGSELIFLED 255

Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
           ||||| |||:|||:|||||||||||    :||:||||||||:||||||||||||||||||||
Db  256 SPDYCLKNISLGLQGTEGRECLQSGKNLSQWERRSCKRLCTDCGLRVEEKKTEISSCNC 315

Qy  333 KFQWCCTVKCDQCRHVVSKYYCAR 356
           ||:|||||||::|| ||| :|||||
Db  316 KFHWCCTVKCEQCQCKQVVIKHFCAR 339
```

RESULT 9
US-09-842-758-47
Sequence 47, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:

APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard A
APPLICANT: Malyankar, Uriel M
APPLICANT: Boldog, Ferenc L
APPLICANT: zerhusen, Bryan D
APPLICANT: Spytek, Kimberly A
APPLICANT: Majunder, Kumud
APPLICANT: Tcherney, Velizar T
APPLICANT: Padigaru, Muralidhara
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine E
APPLICANT: Gangolli, Esha A
APPLICANT: Smithson, Glennda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R
APPLICANT: Taupier, Raymond J
APPLICANT: Grosse, William M
APPLICANT: Edward, Szekeres S
APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006

```
Qy  222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNS 281
           ||:||||||||||:|||||||:||||||:||    |||||||||||||||||:|||| |:
Db  204 MGNYLKAKYDRALKIEMDKRQLRAGNRAEGRWALTEAFLPSTEAELIFLEGSPDYCNRNA 263

Qy  282 SLGIYGTEGRECLQNSHSNTSRWERRSCGRLLCTECGLQVEERKTEVISSCNCKFQWCCTVK 341
           ||.| ||||||||||    :||:||||||| ||:||||||||||||||||||||||:||||||
Db  264 SLSIQGTEGRECLQNARSASRREQRSCGRLCTECGLQVERRAEAVSSCDCNFQWCCTVK 323

Qy  342 CDQCRHVVSKYYCARSPGSAQSLGKG 367
           |::|| |||:|||| : |||:  | |
Db  324 CGQCRRVVSRYYCTRPVGSARPRGRG 349
```

RESULT 8
US-09-842-758-46
Sequence 46, Application US/09842758
Publication No. US20030083244A1
GENERAL INFORMATION:

APPLICANT: Vernet, Corine A. M.
APPLICANT: Fernandes, Elma R
APPLICANT: Gerlach, Valerie
APPLICANT: Shimkets, Richard A
APPLICANT: Malyankar, Uriel M
APPLICANT: Boldog, Ferenc L
APPLICANT: zerhusen, Bryan D
APPLICANT: Spytek, Kimberly A
APPLICANT: Majunder, Kumud
APPLICANT: Tcherney, Velizar T
APPLICANT: Padigaru, Muralidhara
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine E
APPLICANT: Gangolli, Esha A
APPLICANT: Smithson, Glennda
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R
APPLICANT: Taupier, Raymond J
APPLICANT: Grosse, William M
APPLICANT: Edward, Szekeres S
APPLICANT: Alsobrook II, John P
TITLE OF INVENTION: No. US20030083244A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-783
CURRENT APPLICATION NUMBER: US/09/842,758
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/200,158
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/200,613
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,780
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/201,006
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113

PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,007
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,236
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,238
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/201,186
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,474
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/201,508
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 60/220,591
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/232,678
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/263,217
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/265,160
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 47
LENGTH: 357
TYPE: PRT
ORGANISM: Gallus gallus
US-09-842-758-47

Query Match   67.7%;   Score 1379; DB 11; Length 357;
Best Local Similarity 76.5%;   Pred. No. 1.4e-126;
Matches 241; Conservative 37; Mismatches 37; Indels 0; Gaps 0;

Qy   42 SVNNFLITGPRAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATR 101
         ||||||||||||||||:|:||||||||||||||:||||:|||||||||||||||||||||
Db   25 SVNNFLMTGPRAYLIYSSSVAAGAQSGMEECKFQFGWERWNCPESALQLSTHNRLRSATR 84

Qy 102 ETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERIS 161
         |:|||||||:|||||:||||||||||||:|:||||:||||||||:|||||||||||||||
Db   85 ETSFVHAISSAGVMYLTLRNCSLGDFESCGCGDDSRNGRVGGRGWWNGGCSDNVEFGERIS 144

Qy 162 KLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE 221
         |||||:|||||||||||||||||||||:||:||||||||||:||||||||||||::|||
Db 145 KLFVDALETGHDTRALINLHNNEVGRLAVKATMKRACKCHGVSGSCSIQTCWLQLADFRE 204

Qy 222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNS 281
         ||||||||||||||||||||||:||||||||:||||||||||||||||||||||||||:
Db 205 IGNYLKMKYDQAHKLEMDKRMRAGNSADSRGATATFHHVSHTELVFLEDSPDYCTRNA 264

Qy 282 SLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVK 341
         |||||:|||||||||||||||||||:||||||:|||||||:|||||||||||:|:|||:
Db 265 SLGHGTEGRCLQTGKNLSQWERRSCRRLSTECGLKVEERRTEVVSSCNCKFHWCCTVR 324

Qy 342 CDQCRHVSKYYCAR 356
         |:|||||||:|||
Db 325 CEQCRQLVAKHFCAR 339

RESULT 10
US-10-285-976-25
Sequence 25, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leoni, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-13032US

CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 25
LENGTH: 351
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human Wnt-8b
US-10-285-976-25

Query Match   59.5%;   Score 1213; DB 12; Length 351;
Best Local Similarity 63.8%;   Pred. No. 2.6e-110;
Matches 220; Conservative 44; Mismatches 71; Indels 10; Gaps 3;

Qy   26 CLIPIHLCLTFSLFGRSVNNFLITGPRAYLTYTTSVALGAQSGIEECKFQFAWERWNCPE 85
         |::|||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db   11 CLFTCVLQLSHSW---SVNNFLMTGPRAYLIYSSSVAAGAQSGIEECKYQFAWDRWNCPE 67

Qy   86 NALQLSTHNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGGHGW 145
         ||||||||||||||||||:|||||||||||||:|||||||||||:|:||||:|||||||:
Db   68 RALQLSSHGGLRSANRETAFVHAISSAGVMYVTLTRNCSLGDFDNCGCDDSRNGLGGQGW 127

Qy 146 IWGGCSDNVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISG 205
         |||||||||||||||||||:||||||||||||||||||||:|||:|||||||||||:||
Db 128 LWGGCSDNVGFGEAISKQFVDALETGQDARAAMNLHNNEAGRKAVKGTMKRTCKCHGVSG 187

Qy 206 SCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEA 265
         :|||||||||||||||||||||||||||||||||||||:||||:||||:||||||||||
Db 188 SCTTQTCWLQLPEFREVGAHLKEKYHAALKVDLLQ--GAGNSAAARGAIADTFRSISTR 244

Qy 266 ELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTE 325
         |:||||||||||||:||||||||||||||||||||||||||||:|||||||||||:|||:
Db 245 ELVHLEDSPDYCLENKTIGLLGTEGRECLRRGRALGRWELRSCRRLCGDCGLAVEBRRAE 304

Qy 326 VISSCNCKFQWCCTVKCDQCRHVSKYYCARSP----GSAQSLGK 366
         :||||||||||||:|:|||||||||::||:| :|||||||:
Db 305 TVSSCNCKFHWCCAVRCEQCRRRVTKYFCSRAERPRGGAAHKPGR 349

RESULT 11
US-10-005-947-6
Sequence 6, Application US/10005947
Publication No. US20020123103A1
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
TITLE OF INVENTION: Human Wnt Gene
FILE REFERENCE: 99-87
CURRENT APPLICATION NUMBER: US/10/005,947
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: US/09/715,993
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-005-947-6

Query Match   55.8%;   Score 1137.5; DB 14; Length 295;
Best Local Similarity 68.0%;   Pred. No. 5.2e-103;
Matches 202; Conservative 35; Mismatches 57; Indels 3; Gaps 1;

Qy   42 SVNNFLITGPRAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNRLRSATR 101
         ||||||:|||||||:|:|||||||||||||||||:||||:||||||||||||||:||||
Db   2 SVNNFLMTGPRAYLIYSSSVAAGAQSGIEECKYQFAWDRWNCPERALQLSSHGGLRSANR 61

RESULT 12
US-10-029-386-32775
Sequence 32775, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
  APPLICANT: Penn, Sharron G.
  APPLICANT: Rank, David R.
  APPLICANT: Hanzel, David K.
  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR Q
  FILE REFERENCE: AEOMICA-X-2
  CURRENT APPLICATION NUMBER: US/10/029,386
  CURRENT FILING DATE: 2001-12-20
  NUMBER OF SEQ ID NOS: 34288
  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
  SEQ ID NO 32775
  LENGTH: 176
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  OTHER INFORMATION:
  OTHER INFORMATION: MAP TO AC004826.3
  OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.61
  OTHER INFORMATION: SWISSPROT HIT: Q9HJU5, EVALUE 1.00e-105
US-10-029-386-32775

Query Match   100.0%; Score 973; DB 12; Length 176;
Best Local Similarity   100.0%;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 ETSPIHAISSAGVMYIIITKNCSMGDPFENCCGCDGSNNGKTGGHGWIWGGGCSDNVFGFGERIS 161
Db   62 ETAPVHAISSAGVMYLTRNCSLGDFDNCCGCDDSRNGQLGGGQGWLWGGCSSDNVFGEAIS 121
Qy 162 KLFVDSLEKKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFRE 221
Db 122 KQFVDALETGQDARAAMNLHNNEAGRKAVKGTMKRTCKCHGVSGSGCTTQTCWLQLPEFRE 181
Qy 222 MGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEESPDYCTCNS 281
Db 182 VGAHKEKYHAALKVDLLQ---GAGNSAAARGAIADTFRSISTRELVHLEDSPDYCLENK 238
Qy 282 SLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCC 338
Db 239 TLGLLGTEGRECLRRGRALGRWELRSCRRLCGDCGLAVEERRAETVSSCNCKFHWCC 295

RESULT 13
US-10-028-248A-71
Sequence 71, Application US/10028248A
Publication No. US20030235882A1
GENERAL INFORMATION:
  APPLICANT: Shimkets, Richard
  APPLICANT: Pacturajan, Meera
  APPLICANT: Vernet, Corine
  APPLICANT: Casman, Stacie
  APPLICANT: Malyankar, Uriel
  APPLICANT: Shenoy, Suresh
  APPLICANT: Spytek, Kimberly
  APPLICANT: Gangolli, Esha
  APPLICANT: Miller, Charles
  APPLICANT: Boldog, Ferenc
  APPLICANT: Li, Li
  APPLICANT: Taupier Jr, Raymond J
  APPLICANT: Kekuda, Ramesh
  APPLICANT: Smithson, Glennda
  APPLICANT: Zerhusen, Bryan
  APPLICANT: Liu, Xiaohong
  APPLICANT: Colman, Steven
  APPLICANT: Tcherney, Velizar
  APPLICANT: Si, Jingsheng
  APPLICANT: Ding, Shlomit
  APPLICANT: Ediger, Shlomit
  APPLICANT: Stone, David
  APPLICANT: Sciore, Paul
  APPLICANT: Millet, Isabelle
  APPLICANT: Rothenberg, Mark
  TITLE OF INVENTION: No. US20030235882A1e1 Nucleic Acids and Polypeptides and Methods o
  TITLE OF INVENTION: Thereof
  FILE REFERENCE: 21402-222
  CURRENT APPLICATION NUMBER: US/10/028,248A
  CURRENT FILING DATE: 2001-12-19
  PRIOR APPLICATION NUMBER: 60/256619
  PRIOR FILING DATE: 2000-12-19
  PRIOR APPLICATION NUMBER: 60/262959
  PRIOR FILING DATE: 2001-01-19
  PRIOR APPLICATION NUMBER: 60/272408
  PRIOR FILING DATE: 2001-02-28
  PRIOR APPLICATION NUMBER: 60/285189
  PRIOR FILING DATE: 2001-04-20
  PRIOR APPLICATION NUMBER: 60/308039
  PRIOR FILING DATE: 2001-07-26
  PRIOR APPLICATION NUMBER: 60/311266
  PRIOR FILING DATE: 2001-08-09
  NUMBER OF SEQ ID NOS: 211
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 71
  LENGTH: 352
  TYPE: PRT
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: WNT domain
  OTHER INFORMATION: sequence
US-10-028-248A-71

Query Match   35.0%; Score 712; DB 12; Length 352;
Best Local Similarity   44.8%;
Matches 148; Conservative 46; Mismatches 98; Indels 38; Gaps 11;

Qy 189 AVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNS 248
Db   1 AVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNS 60
Qy 249 AEGHWVPAEAFLPSAEAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSC 308
Db   61 AEGHWVPAEAFLPSABAELIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSC 120
Qy 309 GRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCARSPGSAQSL 364
Db 121 GRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCDQCRHVVSKYYCARSPGSAQSL 176

Qy   60 SVALGAQSGIEECKFQFAWRWNCP--ENALQLSTHNR-LRSATRETSFIHAISSAGVMY 116
Db   1 SVSEGAQLAIQECQHQFPRGRWNCSTLDSLNERSVFGKVLKKGTRETAFVVAISSAGVAH 84
Qy 117 IITKNCSMGDFENCCGCDGSN------------NGKTGGHG-WIWGGGCSDNVFGFGERISK 162
Db   85 AVTRACSEGELESCGCDDKRKADERLRIKLEPKGPGPQSSWKWGGCSDNVFGIRFSR 144
Qy 163 LFVDSLEKGK-------DARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWL 214
Db 145 EFVDARRREKLMTKSRDRDARSLMNLHNNEAGRKAVKSHMRECKCHGVSGSCSLKTCWL 204
Qy 215 QLAEFREMGDYLKAKYDQALKIEMDK------RQLRAGNSAEGHWVPAEAFLPSAE---AE 266
Db 205 SLPDFRRVGDLLKEKYDGAIEVENRGKGQRSLSSRKQASALEAANERFKKPTRNQYTD 264
Qy 267 LIFLEESPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEV 326
Db 265 LVYLEKSPDYCERDRETGSLGTQGRVCNKTSKGL-QW-RDGCELLCCGRGYNTEQ-KVER 321
Qy 327 ISSCNCKFQ--WCCTVKCDQCRHVVSKYYC 354
Db 322 TEKCNCKFHNGWCCYVKCEBCTEVVEVHTC 351

RESULT 14
US-10-285-976-15
Sequence 15, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leoni, Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy in Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-13032US
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human Wnt-5b
US-10-285-976-15

Query Match 31.9%; Score 649.5; DB 12; Length 359;
Best Local Similarity 40.8%; Pred. No. 4.6e-55;
Matches 127; Conservative 49; Mismatches 108; Indels 27; Gaps 7;

```
Qy   54 YLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNR-LRSATRETSFIHAISSA 112
            :|: ||:|::||:||  :||  |   |  |:|:|:| :      ::  |:  ::|
Db   65 YQEHMAYIGEGAKTGIKECOHQFRORWNC-STADNASVFGRVMQIGSRETAFTHAVSAA 123

Qy  113 GVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGK 172
        | :  |: :|   || ||:|||:||  | | |||||| :||||:|| | |::||||:|:|
Db  124 GVVNAISRACREGELSTCGCSRTARPKDLPRDWLWGGCGDNVEYGYRFAKEFVDAREREK 183

Qy  173 D------ARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGD 224
                  |:|:||||:||:|||  | |:: |||||||:|||||:| |||||||||:||
Db  184 NFAKGSBEQGRVLMNLQNNEAGRRAVYKMADVACKCHGVSGSCSLKTCWLQLAEFRKVGD 243

Qy  225 YLKAKYDQALKIEMDKR-QLRAGNSABGHWVPAEAAFLPSAEAELIFLEESPDYCTCNSSL 283
        :||:||||: : | :     | :| :|| :| ::   :|||: :|| |  |:|||| :|||
Db  244 RLKEKYDSAAAMRVTRKGRLELVNS--------RFTQPTPEDLVYVDPSPDYCLRNEST 294

Qy  284 GIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCD 343
        | ||| || | ||::  ::  ::| |:|   ::|  :|:  |::    |||:|:||||:|:
Db  295 GSLGTQGRLCNKTSEGMD-----GCELMC--CGRGYNQFKSVQVERCHCKFHWCCFVRCK 347

Qy  344 QCRHVVSKYYC 354
        :| | || |:|
Db  348 KCTEIVDQYIC 358
```

RESULT 15
US-10-295-027-584
Sequence 584, Application US/10295027
Publication No. US20030233350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-0125000US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/350,666
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,394
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 359
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-584

Query Match 31.9%; Score 649.5; DB 12; Length 359;
Best Local Similarity 40.8%; Pred. No. 4.6e-55;
Matches 127; Conservative 49; Mismatches 108; Indels 27; Gaps 7;

```
Qy   54 YLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLSTHNR-LRSATRETSFIHAISSA 112
            :|: ||:|::||:||  :||  |   |  |:|:|:| :      ::  |:  ::|
Db   65 YQEHMAYIGEGAKTGIKECOHQFRORWNC-STADNASVFGRVMQIGSRETAFTHAVSAA 123

Qy  113 GVMYIITKNCSMGDFENCGCDGSNNGKTGGHGWIWGGCSDNVEFGERISKLFVDSLEKGK 172
        | :  |: :|   || ||:|||:||  | | |||||| :||||:|| | |::||||:|:|
Db  124 GVVNAISRACREGELSTCGCSRTARPKDLPRDWLWGGCGDNVEYGYRFAKEFVDAREREK 183

Qy  173 D------ARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTCWLQLAEFREMGD 224
                  |:|:||||:||:|||  | |:: |||||||:|||||:| |||||||||:||
Db  184 NFAKGSBEQGRVLMNLQNNEAGRRAVYKMADVACKCHGVSGSCSLKTCWLQLAEFRKVGD 243

Qy  225 YLKAKYDQALKIEMDKR-QLRAGNSABGHWVPAEAAFLPSAEAELIFLEESPDYCTCNSSL 283
        :||:||||: : | :     | :| :|| :| ::   :|||: :|| |  |:|||| :|||
Db  244 RLKEKYDSAAAMRVTRKGRLELVNS--------RFTQPTPEDLVYVDPSPDYCLRNEST 294

Qy  284 GIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNCKFQWCCTVKCD 343
        | ||| || | ||::  ::  ::| |:|   ::|  :|:  |::    |||:|:||||:|:
Db  295 GSLGTQGRLCNKTSEGMD-----GCELMC--CGRGYNQFKSVQVERCHCKFHWCCFVRCK 347

Qy  344 QCRHVVSKYYC 354
        :| | || |:|
Db  348 KCTEIVDQYIC 358
```

Search completed: January 30, 2004, 13:35:48
Job time : 41 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: January 30, 2004, 13:29:15 ; Search time 23 seconds
(without alignments)
1215.200 Million cell updates/sec

Title: US-09-898-456-7
Perfect score: 2037
Sequence: 1 MLCCIQCLCLVSPFPTLTPC..........SKYYCARSPGSAQSLGKGSA 369

Scoring table: BLOSUM62
Gapop.10.0 , Gapext 0.5

Searched: 367270 seqs, 75744148 residues

Total number of hits satisfying chosen parameters: 367270

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : Pending Patents AA New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1808	88.8	351	1	PCT-US03-37355-58	Sequence 58, Appl
2	1804	88.6	351	6	US-10-451-168-62	Sequence 62, Appl
3	1791	87.9	355	1	PCT-US03-31384-21	Sequence 21, Appl
4	1791	87.9	355	1	PCT-US03-31384-21	Sequence 21, Appl
5	1213	59.5	351	1	PCT-US03-31384-22	Sequence 22, Appl
6	1211	59.5	351	1	PCT-US03-31384-22	Sequence 22, Appl
7	650.5	31.9	391	1	PCT-US03-31384-27	Sequence 27, Appl
8	650.5	31.9	391	1	PCT-US03-31384-27	Sequence 27, Appl
9	649.5	31.9	359	1	PCT-US03-31384-17	Sequence 17, Appl
10	649.5	31.9	359	1	PCT-US03-31384-17	Sequence 17, Appl
11	649.5	31.9	359	5	PCT-US03-976-858-88	Sequence 88, Appl
12	648	31.8	351	1	PCT-US03-31384-15	Sequence 15, Appl
13	648	31.8	351	7	US-60-485-101-623	Sequence 623, App
14	648	31.7	351	7	US-60-485-101-765	Sequence 765, App
15	646	31.7	351	7	US-60-485-101-691	Sequence 691, App
16	644	31.6	351	7	US-60-485-101-691	Sequence 691, App
17	640.5	31.4	360	1	PCT-US03-31384-8	Sequence 8, Appli
18	640.5	31.4	360	1	PCT-US03-31384-8	Sequence 8, Appli
19	640.5	31.4	360	1	PCT-US03-31384-8	Sequence 8, Appli
20	640.5	31.2	338	1	PCT-US03-17512-178	Sequence 178, App
21	636.5	31.2	338	6	US-10-454-246-178	Sequence 178, App
22	636.5	31.2	365	5	PCT-US03-37355-56	Sequence 56, Appl
23	636.5	31.2	365	1	PCT-US03-17512-176	Sequence 176, App
24	636.5	31.2	365	1	PCT-US03-31384-16	Sequence 16, Appl
25	636.5	31.2	365	1	PCT-US03-31384-16	Sequence 16, Appl
26	636.5	31.2	365	6	US-10-474-291-13	Sequence 13, Appl
27	636.5	31.2	365	6	US-10-454-246-176	Sequence 176, App
28	636	31.2	370	1	PCT-US03-37355-50	Sequence 50, Appl
29	636	31.2	370	1	PCT-US03-31384-1	Sequence 1, Appli
30	636	31.2	370	1	PCT-US03-31384-1	Sequence 1, Appli
31	636	31.2	370	7	US-60-505-218-524	Sequence 524, App
32	626	30.7	352	1	PCT-US03-25100-148	Sequence 148, App
33	626	30.7	352	1	PCT-US03-25100-192	Sequence 192, App
34	626	30.7	355	1	PCT-US03-37355-54	Sequence 54, Appl
35	626	30.7	355	1	PCT-US03-31384-13	Sequence 13, Appl
36	626	30.7	355	1	PCT-US03-31384-13	Sequence 13, Appl
37	625	30.7	334	1	PCT-US03-25100-160	Sequence 160, App
38	625	30.7	338	1	PCT-US03-25100-142	Sequence 142, App
39	625	30.7	352	1	PCT-US03-31384-14	Sequence 14, Appl
40	625	30.7	352	1	PCT-US03-31384-14	Sequence 14, Appl
41	625	30.7	352	1	PCT-US03-25100-140	Sequence 140, App
42	625	30.7	352	1	PCT-US03-25100-144	Sequence 144, App
43	625	30.7	352	1	PCT-US03-25100-146	Sequence 146, App
44	625	30.7	352	1	PCT-US03-25100-152	Sequence 152, App
45	625	30.7	352	1	PCT-US03-25100-156	Sequence 156, App

ALIGNMENTS

RESULT 1
PCT-US03-37355-58
; Sequence 58, Application PC/TUS0337355
; GENERAL INFORMATION:
; APPLICANT: Keating et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND TISSUE
; TITLE OF INVENTION: REGENERATION
; FILE REFERENCE: HYDR-PW1-004
; CURRENT APPLICATION NUMBER: PCT/US03/37355
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 58
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-37355-58

Query Match 88.8%; Score 1808; DB 1; Length 351;
Best Local Similarity 98.2%;
Matches 331; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy  33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST  92
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGIEECKFQFAWERWNCPENALQLST  74

Qy  93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGHGWIWGGCSD 152
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGSNNGKTGHGWIWGGCSD 134

Qy 153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 194

Qy 213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy 273 SPDYCYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 255 SPDYCYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy 333 KFQWCCTVKCDQCRHVSKYYCARSPGSAQSLGKGSA 369
        ||||||||||||||||||||||||||||||||||||
Db 315 KFQWCCTVKCDQCRHVSKYYCARSPGSAQSLGKGSA 351
```

RESULT 2
US-10-451-168-62

; Sequence 62, Application US/10451168
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 62
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Patentin Ver. 2.1
US-10-451-168-62

```
Query Match      88.6%;  Score 1804;  DB 6;  Length 351;
Best Local Similarity  97.9%;  Pred. No. 2.1e-137;
Matches  330;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGTEECKFQFAWERWNCPENALQLST 92
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGTEECKFQFAWERWNCPENALQLST 74

Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGDGSNNGKTGGHGWIWGGCSD 152
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGDGSNNGKTGGHGWIWGGCSD 134

Qy  153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
        |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLVVRATMKRTCKCHGISGSCSIQTC 194

Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy  333 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 369
        |||||||||||||||||||||||||||||||||||||
Db  315 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGKGSA 351
```

RESULT 3
PCT-US03-31384-21
; Sequence 21, Application PC/TUS031384
; GENERAL INFORMATION:
; APPLICANT: He, Biao
; APPLICANT: You, Liang
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
; FILE REFERENCE: 023070-12563OPC
; CURRENT APPLICATION NUMBER: PCT/US03/31384
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 10/264,825
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/491,350
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 21
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wingless-type 8A (Wnt-8A) peptide sequence
PCT-US03-31384-21

```
Query Match      87.9%;  Score 1791;  DB 1;  Length 355;
Best Local Similarity  97.9%;  Pred. No. 2.4e-136;
Matches  327;  Conservative  1;  Mismatches  6;  Indels  0;  Gaps  0;

Qy   33 CLTFSLFGRSVNNFLITGPKAYLTYTTSVALGAQSGTEECKFQFAWERWNCPENALQLST 92
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15 CAAFSASAWSVNNFLITGPKAYLTYTTSVALGAQSGTEECKFQFAWERWNCPENALQLST 74

Qy   93 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGDGSNNGKTGGHGWIWGGCSD 152
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75 HNRLRSATRETSFIHAISSAGVMYIITKNCSMGDFENCGCDGDGSNNGKTGGHGWIWGGCSD 134

Qy  153 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLAVRATMKRTCKCHGISGSCSIQTC 212
        |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  135 NVEFGERISKLFVDSLEKGKDARALMNLHNNRAGRLVVRATMKRTCKCHGISGSCSIQTC 194

Qy  213 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 272
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  195 WLQLAEFREMGDYLKAKYDQALKIEMDKRQLRAGNSAEGHWVPAEAFLPSAEAELIFLEE 254

Qy  273 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 332
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  255 SPDYCTCNSSLGIYGTEGRECLQNSHNTSRWERRSCGRLCTECGLQVEERKTEVISSCNC 314

Qy  333 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGK 366
        |||||||||||||||||||||||||||||||||:
Db  315 KFQWCCTVKCDQCRHVVSKYYCARSPGSAQSLGR 348
```

RESULT 4
PCT-US03-31384-21
; Sequence 21, Application PC/TUS031384
; GENERAL INFORMATION:
; APPLICANT: He, Biao
; APPLICANT: You, Liang
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
; FILE REFERENCE: 023070-12563OPC
; CURRENT APPLICATION NUMBER: PCT/US03/31384
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: US 10/264,825
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/491,350
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 21
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wingless-type 8A (Wnt-8A) peptide sequence
PCT-US03-31384-21